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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: January 6, 2003, 14:20:05; Search time 36 Seconds (without alignments)

Title: US-09-454-651B-23
Perfect score: 1149
Sequence: 16.2 Gapext 0.5
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: A_Geneseq_101002:*
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Geneseq_101002:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* /SIDS2/gcgdata/geneseqy-embl/AA1980.DAT:* /SIDS2/gcgdata/geneseqy-embl/AA1980.DAT:* /SIDS2/gcgdata/geneseqy-embl/AA1980.DAT:* /SIDS2/gcgdata/geneseqy-embl/AA1991.DAT:* /SIDS2/gcgdata/geneseqy-embl/AA19
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	otasodamil a nemil	R7-1 HOMO sanion	Himan B7 protein s	Himan D7-7 anticon	Inman B - 2 anciden	Human by mattel	thimen by proceeding	Human B/.1 CO-Stlm	numan b/.1 protein	COLOI ECLAI CUMOUF Himan B lymphocyta
SUMMARIES	ID	AAR67989	AAW38414	AAW67804	AAW73640	AAB37087	AAYGGGG	AAV44289	AAY54920	AAII05121	AAB19959
	DB	16	18	20	20	21	21	21	212	2	22
	Query Match Length DB I	288	288	288	288	288	288	288	288	288	288
~dF	Ouery Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	1149	1149	1149	1149	1149	1149	1149	1149	1149	1149
	Result No.	1	7	e	4	2	9	7	89	6	10

11	114	100.0	288	23	AAE14633	Human B7-1 protein
12	114	。	288	23	AAE15829	co-st
13	114	0	288	23	AAM50795	Human B-lymphocyte
14	114	8	473	18	AAW41415	Human B7.1-murine
15	114	o.	251	20	AAW90208	hB7.19lu-glu solub
16	114	σ.	475	18	AAW38415	Soluble B7-1-1q.
17	114	ດ່	488	20	AAW86004	Human B7-1.5T4.1 p
18	114	٠ م	488	22	AAB83836	Amino acid sequenc
19	114	ດໍ	492	19	AAW42338	4
20	113	o.	480	20	AAW90206	hB7.1Fc soluble fu
21	109	'n.	233	23	AAE15832	Human co-stimulato
22	104	٠.	208	18	AAW35858	
23	76	<u>.</u>	229	22	AAY97780	Soluble porcine B7
2.4	76	Ġ,	229	23	AAE15831	Pig co-stimulatory
2 6	4.		292	21	AAY32283	Feline CD80 (B7-1)
970	7 .		292	21	AAY32276	Cat CD80 (B7-1)-TA
770	7 .		292	23	AA017732	Feline CD80 (TAMU)
200	4/		292	5 23	AAU78119	Feline CD80 (TAMU)
7 6	0 6		767	77	AAY32284	Feline CD80 (B7-1)
000	0, 1	÷.	700	7 7	AAY 322//	Cat CD80 (B7-1)-SY
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9 6	7.7	· ^	304	2 0	AAU/8120	Feline CD80 (SYNTR
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35	561	48.8	306	19	AAR82893	Moneo B7-15 prote
36	26	m	306	16	AAR67990	, a
37	26	m	306	22	AAB19960	٦ ۾
38		~	306	23	AAU99783	ິ
39	26	æ	306	23	AAM50796	onse B
40	26	æ	320	16	AAR82892	
41	52	8	306	20	AAW67805	Œ
42	55	8	306	20	AAW73641	B7-2 antige
43	55	8	306	21	AAB37088	B
44	55	ω.	306	21	AAY99967	DO.
45	467.	0	631	23	AAU75547	B7-
					ALIGNMENTS	
RECITL	,					
R67	586					
ID A	AR67989 st	andard;	Protein	in; 2	88 AA.	
	AAR67989;					
	,					
DT 21	1-AUG-1995	(first	entry)	$\overline{\mathcal{L}}$		
DE H	Human B lym	lymphocyte	antigen	en B7	-1 (hB7-1).	

				vation antigen; CD28; mbrane protein.											400	, racton			
ırd; Protein; 288 AA.		(first entry)	Human B lymphocyte antigen B7-1 (hB7-1).	B lymphocyte antigen; B7-1; B cell activation ligand; T cell surface antigen; transmembrane		Location/Oualifiers	134	/label= signal sequence	/note= "hydrophobic"		/Label= extracellular 243 269	/label= transmembrane	270288	/label= intracellular		8991			186188
KESULT 1 AAR67989 ID AAR67989 standard; xx	AAR67989;	21-AUG-1995 (f	Human B lymphoc	B lymphocyte an ligand; T cell	Homo sapiens.	Key	Protein		,	Domain	Domain		Domain	Min. 11.66	misc-uillerence	Misc-difference	Misc-difference	20.00	Misc-difference

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Human; B7; transfection; mammal; tumour cell; sarcoma; co-stimulation;
T- cell; CD28; CTLA4; ligand; T-lymphocyte response; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence was used in the development of a novel method for screening for compounds that inhibit or enhance binding of CD28
                                                                                                                                                                                                                                                                                                                                                         New xanthene derivatives useful as immunomodulators - e.g. methyl 2-(carboxymethylsulphinyl)-5,7-dichloro-3,8-dihydroxy-6-methyl-9-oxo-9H-xanthene-1-carboxylate.
                                                     Screening; inhibitor; enhancer; binding; CD28; B7-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1149; DB 18;
100.0%; Pred. No. 3.2e-103;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW67804 standard; Protein; 288 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 4; 117pp; English.
                                                                                                                                                                                                                                                                                   Hattori M, Hida T, Kurokawa T,
                                                                                                                                                                                                                           96JP-0047795.
                                                                                                                                                                                                                                                       (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                97EP-0301438
                                                                                                                                                                                                            96JP-0262085
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08-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 216; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 AA;
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                                                                                                                                                                                                              02-OCT-1996;
                                                                                                                                                                                04-MAR-1997;
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                                                                                         Homo sapiens
                                                                                                                      EP79554-A2
                                                                                                                                                  17-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1) GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKWVLTMMSGDMNIWPE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q81371 is in pCDM8 vector. It is derived from lymphoid B cells, cell line Raji, clone no. 13. Its position in the genome is chromosome/segment 3. It was published by Freeman, F.J. et al., J. of Immunology, 143: 8: 2714-2722, 15th October 1989. It can be found in Genbank at Accession no. M27533. The encoded protein, R67989, binds both human CTLA4 and human CD28. It is related to human hB7-2 (see Q81351) and murine hB7 (see Q81372).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful for enhancing or suppressing T-cell mediated immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 288;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1149; DB 16;
100.0%; Pred. No. 3.2e-103;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                   Nadler LM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; pages 111-113; 175pp; English
                                                                                                         /label= see above
35..138
/label= Ig V-set domain
139..236
                                                                                                                                                                       /label= Ig C-set domain
                                                                                                                                                                                                                                                                                                                                                                                                   Greenfield E,
                                                                                                                                                                                                                                                                                                                                                  DAND ) DANA FARBER CANCER INST INC (REPK ) REPLIGEN CORP.
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      Misc-difference 207. 209

Alabel see above 211..213

Alabel see above 211..213
                                                           /256..228
/label= see above
232..234
                                                                                                                                                                                                                                                               94WO-US08423
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Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Freeman GJ, Gray GS,
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-075236/10.
N-PSDB; AAQ81371.
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                                                                  Misc-difference
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Sequence Query Match AAW38414;

RESULT 2 AAW38414 XXXX

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19-AUG-1993; 03-NOV-1993;

26-JUL-1994; 26-JUL-1993;

WO9503408-A 02-FEB-1995

Domain Domain

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Length 288; Indels 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180

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NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216

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AAW73640 standard; Protein; 288 AA

AAW73640 RESULT 4

(first entry)

23-MAR-1999

AAW73640;

Human B7-2 antigen

YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120

27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86

m

Page

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This sequence represents the amino acid sequence of a human B7 protein. The coding sequence can be used to transfect mammalian tumour (sarcoma) cell so that the B7 protein is expressed by the tumour cell and has the ability to co-stimulate T cells and bind cD28 or CTLA4 ligand. The modified tumour cells can be used for inducing an anti-tumour T-ymphocyte response in a subject and are effective against both modified and unmodified tumour cells. The modified tumour cells can also be administered to prevent or inhibit metastatic spread of a tumour or to prevent or inhibit recurrence of a tumour following therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wew incollised/tumour cells - transfected in order to express a T cell costimulatory molecule which allows the induction of an anti-tumour response by T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ostrand-Rosenberg
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                                                                                                                                            /note= "Asn is N-glycosylated"
98..100
                                                                                                                                                                                                                             /note= "Asn is N-glycosylated"
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226..228
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                                           .242
.te= "extracellular domain"
                                                                                                                                                                                                                                                                          "Asn is N-glycosylated"
                                                                                  "transmembrane domain"
                                                                                                         "intracellular domain"
                                    "mature B7 protein"
                                                                                                                                                                                                                                                                                                                         "Ig V-set domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Column 31-34; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                 /note= "Ig C-set domain"
            "signal peptide"
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236..234
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270..288
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                                                                                                                                                                                                       /note=
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(REPK ) REPLIGEN CORP
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                        Protein
 Peptide
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O
                                                                                                                                                                                                                                                                                                             Domain
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antigen; mammalian tumour cell; T cell costimulation; CD28 ligand;

therapy; T-cell response; human.

CTLA4 ligand; Homo sapiens

JS5861310-A 19-JAN-1999 (DAND) DANA FARBER CANCER INST INC.

95US-0456104 93US-0147773 95US-0456104

30-MAY-1995;

30-MAY-1995; 03-NOV-1993; Nadler LM;

Gray GS,

Freeman GJ,

WPI; 1999-130394/11

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method of the invention. The method is for transfecting an isolated mammalian tumour cell with an exogenous nucleic acid molecule encoding a mammalian B7-2 molecule, where the B7-2 molecule is expressed in the tumour cell is capable of costimulating a T cell and is capable of binding a CD28 or CTLA4 ligand. The method is useful for treating tumours by stimulating a T-cell response against tumour cells in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                       Tumour cell transfected to express B7-2 molecule - useful for tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is the human B7-2 antigen, which can be used in the
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1149; DB 20; 100.0%; Pred. No. 3.2e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 37-40; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                   therapy by stimulating T-cell response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
Les 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60

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Gaps

; 0

100.0%; Score 1149; DB 20; Length 288; 100.0%; Pred. No. 3.2e-103; Indels 0; Mismatches 0; Indels 0;

Local Similarity 100.0%; les 216; Conservative C

Matches

288 AA;

Sequence Query Match

treatment

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The invention relates to an isolated nucleic acid molecule encoding a first fusion protein comprising a first nucleotide sequence encoding a first peptide, and a second nucleotide sequence encoding a second peptide.

The first nucleotide sequence hybridizes in 6 X sodium chloride/sodium citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C to a portion of a nucleotide sequence which encodes a human or murine is lamphocyte antigen (B7-2) extracellular domain. The first peptide has catracellular domain of a human B7-2 peptide has an amino acid sequence that is identical or at least 50% identical with the cextracellular domain of a human B7-2 peptide (AAB37085). The second peptide is especially an immunoglobulin constant region. This sequence comparison with the B7-2 sequence. The human B7-2 protein is an example constants on with the B7-2 sequence. The human B7-2 protein is an example of a first peptide sequence of the invention. The nucleic acid molecules are useful in various expression vectors to direct synthesis of the corresponding proteins or peptides in a variety of hosts, particularly centearyotic cells, e.g. mammalian or insect cell culture. The nucleic acid molecules corresponding proteins or peptides in a variety of a mammalian cell, e.g. tumour cell (sarcoma) or an antigen presenting cell (arcoma) or an antigen presenting cell. (macrophage). The fusion proteins or peptides are useful for enhancing culturer sexponses, e.g. in situations of tissue, skin or organ transplantation, or in graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for enhancing or suppressing T cell-mediated immune responses, especially during tissue, skin or organ transplantation, or in graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen; extracellular domain; CTLA4; immunoglobulin constant region; immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage; T cell-mediated immune response; transplantation; vaccination.
ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                        Gray GS, Greenfield E;
                                                                                                                                                          NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                  Disclosure; Column 87-90; 83pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB37087 standard; Protein; 288 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human B lymphocyte antigen B7-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0101624.
93US-0109393.
93US-0147773.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REPK ) REPLIGEN CORP.
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N-PSDB; AAC84051.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6130316-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB37087;
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                                                                                                                                                                                                                                                                                                                                                             RESULT 5
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The proteins are also useful for enhancing the efficacy of vaccination against a variety of pathogens, and may also be used to upregulate an immune response against a particular pathogen during an infection or against a tumour in a tumour-bearing host.
                                                                                                                                                                                                                                                                                                                                                                                           ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                      17 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86
                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                              1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF
                                                                                                                                                                                   100.0%; Score 1149; DB 21; Length 288; 100.0%; Pred. No. 3.2e-103; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B7; human; B cell activation antigen; B lymphocytes; autoimmune disease; rheumatoid arthritis; multiple sclerosis; herpes simplex; influenza; common cold; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "N-linked glycosylation site"
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107..209
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'note= "N-linked glycosylation site"
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/note= "N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-linked glycosylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane_domain
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/label= Intracellular_domain
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/label= Extracellular_domain
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/label= "Ig V-set domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY99966 standard; Protein; 288 AA
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/label= "
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                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                 Best Local Similarity
Matches 216; Conserv
                                                                                                                                           288 AA;
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                                                                                                                                           Sequence
                                                                                                                                                                                              Query Match
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metabolism; cancer; autoimmune disease; glycoprotein;
              neurodegenerative disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 AA;
                                                                                                                                                                                                                                     N-PSDB; AAZ29320
   mitochondrial
                                     Homo sapiens
                                                          W09953953-A2
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                                                                                                       30-MAR-1999;
                                                                                                                              17-APR-1998;
29-JUL-1998;
                                                                                                                                                     24-SEP-1998;
                                                                                 28-OCT-1999
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nes 216;
                                                                                                                                                                                                Newell MK;
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                                                                                                                                                                                                                                                  The present sequence is the unique human B cell activation antigen B7 protein. The cDNA encoding this sequence was isolated from a Burkitt lymphoma cell line cDNA library. Selection of cDNA clones was based on expression of B7, as detected by the anti-B7 monoclonal antibody. The human B7 cDNA was used in hybridisation analysis to isolate the murine B7 cDNA (see AAA61329). The B7 nucleic caid sequences may be used to generate transgenic, knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The expressed B7 protein is useful for enhancing or blocking activated T cell mediated immune responses and immune of autorium. Modification of B7 expression is useful in the treatment of autoriumne diseases (e.g. rheumatoid arthritis or multiple sclerosis), herpes simplex, influenza, the common cold and HIV. It is also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human B7.1 co-stimulatory molecule; antigen presenting cell; immune response; cell surface receptor; Major histocompatibility co MHC classII; proton motor force; mitochondrial membrane potential;
                                                                                                                                                                                              New polynucleotides encoding a B7 activation antigen, useful for regulating T cell mediated immune responses or viral diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1149; DB 21; Length 288; 100.0%; Pred. No. 3.2e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                       Freedman AS
                                                                                                                (DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human B7.1 co-stimulatory molecule.
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                                                                                                                                                                                                                                Claim 1; Fig 4; 36pp; English
                                                       93US-0153262.
                                                                              91US-0751306
                                                                                        90US-0591300
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Matches 216; Conservative
                                                                                                                                       Freeman GJ,
                                                                                                                                                            WPI; 2000-422081/36
                                                                                                                                                                                                                                                                                                                                                                                                                                 288 AA;
                                                                                                                                                                         N-PSDB; AAA61328
                                                                             28-AUG-1991;
                                                       15-NOV-1993;
                                                                                         01-OCT-1990;
         US6071716-A
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                                06-JUN-2000
                                                                                                                                      Nadler LM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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The present sequence is human B7.1 co-stimulatory molecule. This is a glycoprotein on the surface of antigen presenting cells. This is involved in stimulation of an immune response by its ability to interact with various immune cell surface receptors. The regulation of cell surface expression of MHC classII and co-stimulatory molecule B7 can be manipulated by regulating the intracellular dissipation of proton motor force which can be assessed in terms of mitochondrial membrane potential. These methods can be used for regulating cell growth and division to control disease processes by manipulating mitochondrial metabolism and the expression of cell surface immune proteins. They can be used for treating diseases associated with excessive cellular division, aberrant differentiation, and premature cellular death, e.g. cancers, autoimmune diseases, neurodegenerative disorders etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           products for treating cancers, autoimmune diseases or neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of cell surface and membrane characteristics for developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1149; DB 21; Length 288; 100.0%; Pred. No. 3.2e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 115; 123pp; English.
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                                                                    98US-0094519.
98US-0094519.
98US-0101580.
99WO-US06874
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This sequence represents the human B7.1 protein sequence.

The invention relates to an isolated nucleic acid construct (I) comprising a region encoding an interleukin-12 (IL-12) fusion protein (comprising an IL-12 p35 subunit, an IL-12 p40 subunit and a linker peptide (joining the subunits)) and a region encoding a B7 protein. (I) may be used to produce IL-12 fusion proteins according to standard recombinant DNA methodologies. The fusion proteins may be produced either in vitro in a fermentation culture or in vivo as part of a gene therapy protocol (in this case (I) is used to transform a patients cells, which then secrete the functional polypeptide to supplement the patients own production of IL-12 or to rectify mutations which lead to the expression of inactive polypeptides). The fusion proteins produced in this way may be used to treat any disease which responds to IL-12 such as tumours of eused to treat any disease which responds to IL-12 such as tumours and melanomas) and in particular, tumours of the blood cervical tumours and melanomas) and in particular, tumours of the blood such as leukaemia. Alternatively, the polypeptides may be used as antigens in the production of antibodies to IL-12 and to assay for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agonists and antagonists of its activity. The antibodies and antagonists may be used to inhibit the activity of IL-12. (I) may also be used diagnostically as a probe which hybridizes to sequences encoding IL-12 and the antibodies may be used to detect the presence of IL-12 the appropriates in Samples. They may be used diagnostically to quantitate the expression of the polypeptide by patients and hence which subjects may be in need of restorative therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid constructs encoding interleukin-12 fusion proteins useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206
                                          Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
IL-12 p40 subunit; gene therapy; tumour; leukaemia; B7.1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for treating leukemia and other cancers -
                                                                                                                                                                                                                                                                                                                                                                                         Prentice HG, MacDonald ID;
                                                                                                                                                                                                                                                                                                                                            (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Fig 10; 73pp; English.
Human B7.1 protein sequence.
                                                                                                                                                                                                                                                  96US-0751767
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Matches 216; Conservative
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                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                  08-NOV-1996;
                                                                                                                                                                                                                                                                                               08-NOV-1996;
                                                                                                                                                         US5994104-A.
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The invention relates to a composition for stimulating an immune response in a patient having an adenocarcinoma or colorectal cancer. The composition comprises an allogeneic tumour cell selected from SW620 cell, coll 205 cell and SW403 cell, and a physiological carrier. The allogeneic cell stimulates an immune response to an autologous tumour cell in the patient. The composition is useful for stimulating an immune response to a autologous tumour cell in the patient. The use of allogeneic tumour cells provides a generic adenocarcinoma. The use of allogeneic tumour cells provides a generic source of anityen that can be administered to a variety of patients, in contrast to using autologous tumour cells, which must be isolated from each individual patient. The allogeneic cells are suitable as a cancer vaccine and can stimulate an immune response against autologous tumour cells of a cancer patient. The present sequence represents the amino acid sequence of colorectal tumour antigen CD80 used in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising an allogeneic tumour cell, useful for stimulating an immune response in a patient having an adenocarcinoma, especially useful for treating colorectal, breast, lung or prostate
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                                                                                                                                                                              Colorectal cancer; immunostimulant; cytostatic; immune response; adenocarcinoma; allogeneic tumour cell; SW620 cell; COLO 205 cell; SW403 cell; colon; breast; lung; prostate; cancer; vaccine; tumour antigen CD80.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gold
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                                    AAU05121 standard; Protein; 288 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KIMM-) KIMMEL CANCER CENT SIDNEY. (IMMU-) IMMUNE RESPONSE CORP.
                                                                                                                                               Colorectal tumour antigen CD80.
                                                                                                                                                                                                                                                                                                                                                                                            26-JAN-2001; 2001WO-US02731.
                                                                                                                                                                                                                                                                                                                                                                                                                               27-JAN-2000; 2000US-0178498.
28-FEB-2000; 2000US-0185335.
                                                                                                              (first entry)
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Best Local Similarity 100.
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shawler DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-502616/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 AA;
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                                                                                                                                                                                                                                                                                                                   WO200154716-A2.
                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                            24-OCT-2001
                                                                                                                                                                                                                                                                                                                                                       02-AUG-2001
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                                                                       AAU05121;
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RESULT 9
AAU05121
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121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENĠEELNAINŤIVSQDPETELYAVSSKLDF 180
           CTLA4; tumour; melanoma; neuroblastoma; leukaemia; carcinoma;
                                                                                                                                                                       B7; B lymphocyte; antigen; T cell costimulatory molecule;
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                                                                                                                                                                                                                                                                                                                                            .236
e= "immunoglobulin C-set domain"
                                                                                                                                                                                                                                                                                                                                    "immunoglobulin V-set domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Asn is N-glycosylated"
232..234
/note= "Asn is N-glycosylated"
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207..209
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                                             /note= "transmembrane domain" 270..288
                                   NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                               "extracellular domain"
                                                                                                                                                                                                                                                                                                                    /note= "intracellular domain"
                                                                                                                                                                                                                                         ...34
/label= Signal_peptide
                                                                                                                                                                                                                                                               /label= Mature_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                  AA.
                                                                                               AAB19959 standard; Protein; 288
                                                                                                                                                                                        metastasis; antitumour; therapy
                                                                                                                                                     Human B lymphocyte antigen B7.
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                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                              .55
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186..18
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226..22
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                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                   19-MAR-2001
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Nadler LM;
                                                                                                                  AAB19959;
                                                                                                                                                                                                                                   Peptide
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                                   181
                                                    207
                                                                               RESULT 10
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histocompatibility complex (MRC) class I and/or class II molecules, or in which expression of an MRC associated protein, the invariant chain, is inhibited are also disclosed. The modified tumour cells are used to treat a patient with a tumour, preventing or inhibiting metastatic spread or tumour recurrence. The tumour may be a method so a neuroblastoma, a leukaemia or a carcinoma. A method for specifically inducing a CD4+ T cell response against a tumour, and a method for treating a tumour by modification of tumour cells in vivo are also disclosed. The treatment methods increase the immunogenicity of the tumour cell in vivo. The antitumour T cell-mediated immune response is effective both against the modified tumour cells and the unmodified tumour cells from which the modified cells were derived. Thus, the effector phase of the antitumour response induced by the modified tumour cells is not dependent upon expression of a costimulatory molecule on the tumour cells.
                                      Modifying tumor cell for treating tumors, reducing metastatic spread, inhibiting recurrence of tumor and increasing immunogenicity, involves transfecting tumor cells with a nucleic acid encoding B7 molecule -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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                                                                                                                                                                  The present sequence is that of human lymphocyte antigen B7, a T cell costimulatory molecule that binds to CD28 and CTLA4. Tumour cells modified to express a T cell costimulatory molecule, especially B7, are disclosed. The tumour cells are modified by transfection with a nucleic acid encoding the T cell costimulatory molecule, by using an agent which induces or increases expression of the T cell costimulatory molecule on the tumour cell surface, or by coupling the T cell costimulatory molecule to the tumour cell surface, or surface. Tumour cells further modified to express major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T cell; CD3; accessory molecule; CD28; cancer; infectious disease; immunotherapy; human immunodeficiency virus; HIV infection; cytokine; human; B7-1; CD80.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1149; DB 22; Length 288; 100.0%; Pred. No. 3.2e-103; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NMTINHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Column 31-34; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Best Local Similarity 100.
Matches 216; Conservative
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N-PSDB; AAA89224
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The invention relates to a method of inducing T cell population to proliferate for use in therapy comprising activating T cells by contacting T cells in vitro with anti-CD3 antibody which is immobilised on solid phase surface, and stimulating accessory molecule on T cell surface in vitro with anti-CD28 antibody, or stimulatory form of natural ligand for CD28 such as B7-1 or B7-2. The method is useful for inducing a population of T cells to proliferate in sufficient numbers for use in therapy e.g., for treating cancer or an infectious disease. The method can be used to selectively expand the population of CD28*, CD4*, CD4*, CD8*, CD2*, TCD28RA* T cells for immunotherapy. The T cell population resulting by the method can be genetically transduced and used for immunotherapy or can be used for in vitro analysis of infectious agents such as human immunodeficiency vitrus (HIV). Proliferation of a population of CD4*+ T cells obtained from an individual infection. Following the expansion of the T cells to sufficient numbers, the expanded T cells are restored to the individual. Also CD4*+ T cells expanded by the above mentioned is useful for treating HIV infection in an individual. A population
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inducing T cell population to proliferate, useful in cancer therapy, comprises activating T cells by contacting T cells in vitro with immobilized anti-CD3 antibody and stimulating accessory molecule on T
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note= "Asn is N-glycosylated"

211..213
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/note= "Asn is N-glycosylated"
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226..228
/note= "Asn is N-glycosylated"
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/label= Transmembrane_domain
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                                                                        label = Extracellular_domain
                                         "Mature B7-1 protein"
                                                                                                                                                                                                                       "Ig C-set domain"
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                                                                                                    "Ig V-set domain"
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/label= Signal_peptide
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/note= "
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of tumour-infiltrating lymphocytes can be obtained from an individual afflicted with cancer and the T cells stimulated to proliferate to sufflicient numbers and restored to the individual. The supernatants from
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                                                  cultures of T cells expanded from above mentioned method are useful as entite source of cytokines and can be used to sustain T cells in vivo or ex vivo. Stimulating and expanding a population of antigen specific T cells are useful in therapeutic conditions where it is desirable to upregulate an immune response. The T cell proliferation occurs in the absence of exogenous growth factors or accessory cells. The present sequence is human B7-1 (CD80) transmembrane protein used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; vaccine; immunostimulatory molecule; interferon; IFN; therapy; antigen presentation; vaccine; tumourigenesis; cancer; cytostatic; antitumour; antibacterial; virucide; fungicide; protozoacide; B7-1.
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                                                                                                                                                                                                                                                                                                                                                                                     ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human co-stimulatory molecule, B7-1 protein.
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                                                                                                                                                                                                                                                                        Conservative
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Matches 216; Conserv
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                                                                                                                                                                       Invention.
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The present invention relates to a composition of matter comprising an immunostimulatory molecule and animal cells cultured in the presence of at least one interferon (IFN) for a time and under conditions sufficient to enhance the antigen presenting function of the cells. The invention is used as vaccine. The composition is useful for treatment and/or prophylaxis of tumourigenesis, cancer, viral, bacterial, fungal and protozoal infections. The composition which comprises the soluble immunostimulatory molecule and the cultured animal cells is administered separately, sequentially or simultaneously to the patient. The present sequence is human co-stimulatory molecule, B7-1 protein.
                                                                                                                                                                                                                                                                                                          61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                     87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 146
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                                                                                                                                                                                            100.0%; Score 1149; DB 23; Length 288; 100.0%; Pred. No. 3.2e-103; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B-lymphocyte antigen B7; human; T-cell costimulatory molecule; tumour; sarcoma; lymphoma; melanoma; neuroblastoma; leukaemia; carcinoma; cancer; metastasis; gene therapy.
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186..188
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The present sequence is that of human B-lymphocyte antigen B7, a member of the immunoglobulin superfamily with unique expression on activated and neoplastic cells. The invention provides tumour cells modified to express a T-cell costimulatory molecule, such as a CD28 and/or CTLA4 ligand, preferably B-lymphocyte antigen B7. The tumour cells are modified by transfection with nucleic acid encoding the T-cell costimulatory molecule, by using an agent which on the tumour cell surface or by coupling T-cell costimulatory on the tumour cell surface or by coupling T-cell costimulatory molecule on the tumour cell surface or by coupling T-cell costimulatory molecule or the tumour cell surface. The tumour cells may be class I and/or class II molecules or have an WHC associated protein, the invariant chain, inhibited. The modified tumour cells are used to treat a patient with a tumour, preventing or inhibiting metastatic spread of a tumour or preventing or inhibiting recurrence of a tumour. Modification of tumour cells in vivo makes them capable of triggering a costimulatory signal in T-cells. The tumour cell is preferably a sarcoma, lymphoma, melanoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic
                                                                                                                                                                                                                                                                                                                                                                                     Nadler LM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                An isolated mammalian tumour cell transfected with an exogenous nuclacid molecule encoding a mammalian B7 molecule which can be used in methods for treating a patient with a tumour and preventing or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1149; DB 23; Length 288; 100.0%; Pred. No. 3.2e-103; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                 Baskar S, Glimcher LH, Freeman GJ,
207..209
/note= "Asn is N-glycosylated"
                                                  /note= "Asn is N-glycosylated" 226..228
                                                                               /note= "Asn is N-glycosylated" 232..234
                                                                                                                      /note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                              DANA FARBER CANCER INST INC.
UNIV MARYLAND BALTIMORE COUNTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuroblastoma, leukaemia or carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Column 31-34; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibiting metastatic growth
                                                                                                                                                                                                                                                          93US-0147772.
98US-0159135.
                                                                                                                                                                                                                           99US-0450798
                                    211..213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                            HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                             Ostrand-Rosenberg S,
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-138256/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABA91632
 Modified-site
                                    Modified-site
                                                                  Modified-site
                                                                                                    Modified-site
                                                                                                                                                       US6319709-B1
                                                                                                                                                                                                                      29-NOV-1999;
                                                                                                                                                                                                                                                                          23-SEP-1998;
                                                                                                                                                                                                                                                          03-NOV-1993;
                                                                                                                                                                                       20-NOV-2001
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181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216

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AAW90208 standard; Protein; 251 AA.
                                                                                        10-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                               AAW90208;
                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                Domain
          RESULT 15
                        AAW90208
                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is the human B7.1-murine A5B7 F(ab')2 fusion protein (AB7), and is an example of the antibody of the invention. The antibody is an anti-CBA (carcinoembryonic antibody antibody (preferably 806.077 Ab). Host cells or transgenic organisms transformed with DNA encoding the antibody, are used to make the antibody or conjugate. The conjugate is used in a medicament suitable for intravenous administration. The conjugate can be used for cancer therapy, selectively killing tumour cells. The antibody can be used for in vivo or in vitro
                                                                                                                                                                                     Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy; cancer diagnosis; complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYMQKEKKMVLTMMSGDMNIMPE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1149; DB 18; Length 473; 100.0%; Pred. No. 6.3e-103; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-carcinoembryonic antigen antibody 806.077 Ab - used for diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reference Example 3; Page 190-193; 208pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NMTINHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human B7.1-murine A5B7 F(ab')2 fusion protein.
207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
                                                                                AAW41415 standard; Protein; 473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               Emery SC;
                                                                                                                                                                                                                                                                                                                                   97WO-GB01165.
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                                                                                                                                       02-JUN-1998 (first entry)
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                                                                                                                                                                                                                                   Chimeric - Homo sapiens.
Chimeric - Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               Copley CG, Edge MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI: 1997-558987/51
                                                                                                                                                                                                                                                                                                                                                                                                     (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV17340
                                                                                                                                                                                                                                                                            WO9742329-A1,
                                                                                                                                                                                                                                                                                                                                   29-APR-1997;
                                                                                                                                                                                                                                                                                                                                                             14-FEB-1997;
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                                                                                                                                                                                                                                                                                                       13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                             AAW41415;
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                                                        RESULT 14
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIXWQKEKKMVLTMMSGDMNIWPE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New molecules which bind B7.1 and B7.2 - useful to prevent and treat
                                                                                                                                                                                                                                                                            /note= "human B7.1 (mature protein) extracellular
                               B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86; T cell activation; inhibitor; graft versus host disease; transplant rejection; allograft rejection; autoimmune disease; allergy; therapy; human; hB7.1glu-glu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.7%; Score 1146; DB 20; Length 251; 99.5%; Pred. No. 5.1e-103; Live 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                     /note= "potential eukaryotic secretory signal
                                                                                                                                                                                                                                                                                                                                   /note= "Glu-Glu detection/purification tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune diseases including allograft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sablon E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3.1.2; Fig 4; 182pp; English.
hB7.1glu-glu soluble fusion protein.
                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                           peptide"
                                                                                                                                                                                                                                                                                                      domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lorre K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-EP03791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97EP-0870092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                 Chimeric - Homo sapiens.
Chimeric - synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                                              35..242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 215; Conserv
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Search completed: January 6, 2003, 14:24:07 Job time : 38 secs

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Sequence 2, Application US/08147772 Patent No. 5858776 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: USA
02109
                                                                                                                                                                       US-08-147-772-2
Sequence 6, Appli
Sequence 29, Appli
Sequence 29, Appl
Sequence 2, Appl
Sequence 19, Appli
Sequence 19, Appli
Sequence 19, Appli
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Sequence 2, Appli
Sequence 13, Appl
Sequence 19, Appl
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Sequence 6, Appli
                                               January 6, 2003, 14:23:30 ; Search time 14 Seconds (without alignments) 453.954 Million cell updates/sec
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Sequence 17, 8
Sequence 17, 8
Sequence 2, Ag
Sequence 2, Ag
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Sequence 131,
Sequence 36,
Sequence 14,
                                                                                                                                                                                                                                                                                                                                               Sequence 23,
                                                                                          ......LRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1
Sequence 1
Sequence 1
Sequence 1
Sequence 1
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Compugen Ltd
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US-08-479-744A-29
US-08-280-757B-29
US-09-159-135-2
US-08-205-697A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-630-172-15
US-09-375-419-15
US-09-651-200-16
US-09-651-200-15
US-08-205-697A-17
US-08-702-525-17
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US-08-456-104-6
US-08-101-624-23
US-08-751-767A-6
                                                                                                                                          Fotal number of hits satisfying chosen parameters:
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US-09-460-384-36
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US-08-205-697A-2
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US-09-651-200-13
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US-09-450-798-2
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                                                                                                                              262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                              SUMMARIES
       GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                            US-09-454-651B-23
1149
1 GLSHFCSGVIHVTKEVKEVA.
                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
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111499
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4, Appli
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                    Sequence 8, A Sequence 8, A Sequence 25, A Sequence 31, Sequence 31, Sequence 4, A Sequence 9, A Sequence 9, A Sequence 9, A Sequence 11, Sequence 11, Sequence 63, Sequence 63, Sequence 63, Sequence 63,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sortand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Baskar, Laurie H.
APPLICANT: Glincher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
NUMBER OF SOUTENES: 4
CORRESPONDENCE ADDRESS: 4
CORRESPONDENCE ADDRESS: ADDRESS: 1
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: -34 to -1 IDENTIFICATION METHOD: amino terminal sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/147,772
FILING DATE:
PCT - US95 - 02576 - 2
US - 08 - 14 7 772 - 4
US - 08 - 165 - 104 - 8
US - 08 - 101 - 624 - 25
US - 08 - 133 - 262 - 4
US - 08 - 479 - 744A - 31
US - 09 - 155 - 135 - 4
US - 09 - 155 - 135 - 4
US - 09 - 155 - 175 - 9
PCT - US95 - 697A - 9
US - 08 - 702 - 525 - 9
PCT - US95 - 02576 - 9
US - 08 - 205 - 697A - 1
US - 08 - 205 - 697A - 1
US - 08 - 205 - 697A - 1
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US - 08 - 205 - 697A - 1
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US-08-702-525-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION.
FILING DATE:
ATTONEY AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: signal sequence
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LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEY: N-linked glycosylation
ION: 55 to 57
IFICATION METHOD: similarity with known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 64 to 66 ... IDENTIFICATION METHOD: SIMILARITY WITH Known IDENTIFICATION METHOD: sequence
                                                                                                                         similarity with known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
INDETIFICATION METHOD: Similarity with known
IDENȚIFICATION METHOD: Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
LOEATICON: 173 to 175
LOEATICATION METHOD: Similarity with known
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: Similarity with known
IDENTIFICATION METHOD: Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFICATION METHOD: similarity with known IFICATION METHOD: sequence
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LOCATION: 105 to 202
LIDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
  soluble protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: N-linked glycosylation LOCALION: 19 to 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: N-linked glycosylation
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                                                                     NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similari
IDENTIFICATION METHOD: sequence
IDENTIFICATION METHOD: soluble OTHER INFORMATION: hydrophobic
                                                                                                                                                                                               NAME/KEY: transmembrane domain LOCATION: 209 to 235
                                                                                                                                                                                                                                                                                                                           NAME/KEY: intracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHITMAN, JAMES F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 55 to 57
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDEN
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APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE NUMBER OF SEQUENCES: 8
NUMBER OF SEQUENCES: ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREFT: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                      1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
: NADLER, LEE M.
B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                  100.0%; Score 1149; DB 2; Length 288; 100.0%; Pred. No. 5.5e-113; tive 0; Mismatches 0; Indels 0
                                                                                                       ; PAGES: 2714-2722
; DATE: 15-OCT-1989
; RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-147-772-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NMTINHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                               JOURNAL: The Journal of Immunology VOLUME: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08456104
Patent No. 5861310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Mandragouras, Amy I
                                                                                                                                                                                                                                                                            Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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ZIP: 02109
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    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-456-104-6
                        TITLE:
TITLE:
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288 amino acids

LENGTH:

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                                                                                                                                                                                                                                                                                                                                                                                         61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                        27 GLSHFCSGVIHVTKEVKEVKEVATLSCGHNVSVEELAQTRIYMQKEKKMVLTMMSGDMNIWPE 86
                                                                                                                                                              Gaps
                                                                                                                                                                                                          1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                              ;
                                                                                                              Query Match 100.0%; Score 1149; DB 2; Length 288; Best Local Similarity 100.0%; Pred. No. 5.5e-113; Matches 216; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray S.
TITLE OF INVENTION: No. 5942607el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/101,624
FILING DATE: 26-7UL-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
BITLY CATON NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23, Application US/08101624 Patent No. 5942607 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 288 amino acids
amino acid
         ; TOPOLOGY: linear
) MOLECULE TYPE: protein
US-08-456-104-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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CITY: Boston
STATE: Massach
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US-08-101-624-23
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amino terminal sequencing of
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LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                       NAME/KEY: transmembrane domain
LOCATION: 209 tO 255
ENERTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity with known sequence
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                                                                                                                                                               similarity with known sequence
                                                                                                                                                                                                                                                                                                                                                                                                          similarity with known sequence
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                                                 soluble protein
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LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: N-linked glycosylation LOCATION: 19 to 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity
IDENTIFICATION METHOD: sequence
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LOCATION: 152 to 154
IDENTIFICATION METHOD: similarit;
IDENTIFICATION METHOD: sequence
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LOCATION: 173 to 175
IDENTIFICATION METHOD: SIMILARILY
IDENTIFICATION METHOD: sequence
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LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarit:
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: N-linked glycosylation
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LOCATION: 236 to 254
IDENTIFICATION METHOD: similari
IDENTIFICATION METHOD: sequence
                                                                     OTHER INFORMATION: hydrophobic
                                                                                                                  NAME/KEY: extracellular domain
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AUTHORS: FREEMAN, GORDON J.
AUTHORS: SEGIL, JEFFREX M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Ig V-set domain LOCATION: 1 to 104
LOCATION: -34 to -1
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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US-08-751-767A-6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                            1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                 AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: WHITMAN, JAMES F.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                        Length 288;
                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                          PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 23: From -26 to 262
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2 IP: 22201

COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996

**TACSTELOGION: 536
                                                                                                                                                                                                                                   100.0%; Score 1149; DB 2;
100.0%; Pred. No. 5.5e-113;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08751767A Patent No. 5994104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFRENCE/CDCKET NUMBER: 117-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                        Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARLINGTON
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COUNTRY: U
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                                                                                                                                                                                                 US-08-101-624-23
                                                                                                                           ISSUE:
PAGES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA Encoding B7, A New Member TITLE OF INVENTION: Of The 1gG Superfamily With Unique Expression On TITLE OF INVENTION: Activated And Neoplastic B Cells.

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                               121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                               Gaps
                                                                                                      1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                            27 GLSHFCSGVIHVTKEVKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86
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                 Length 288;
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                                                             Indels
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IDENTIFICATION METHOD: amino terminal sequencing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage COMPUTER: IBM Personal System 2; Model 30
                   Score 1149; DB 2;
Pred. No. 5.5e-113;
                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: The Dana-Farber Cancer Institute 44 Binney Street
                                                                                                                                                                                                                                                                                                                                                           181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Scor.
100.0%; Pred. No. . . 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/751,306
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: HART, JULIA D.
REGISTRATION NUMBER: 33132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: DFCI-116.1 TELECOMMUNICATION INFORMATION: TELEPHONE: (203) 255-8900 TELEPHONE: (203) 259-2846 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-153-262-2
Sequence 2, Application US/08153262
Patent No. 6071716
GENERAL INFORMATION:
APPLICANT: FREEMAN, GORDON J.
APPLICANT: FREEMAN, ARNOLD S.
APPLICANT: RADLER, LEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: signal sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 288 amino acids TYPE: amino acid
                     Query Match 100.0
Best Local Similarity 100.0
Matches 216; Conservative
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DESCRIPTION: B cell a
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STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 02115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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NAME/KEY: IG C-set domain LOCATION: 105 to 202 IDENTIFICATION METHOD: similarity with known IDENTIFICATION METHOD: sequence PUBLICATION INFORMATION: LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence NAME/KEY: N-linked glycosylation LOCATION: 198 to 200 IDENTIFICATION METHOD: similarity with known IDENTIFICATION METHOD: sequence LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence NAME/KEY: intracellular domain LOCATION: 236 to 254 IDENTIFICATION METHOD: similarity with known IDENTIFICATION METHOD: sequence NAME/KEY: N-linked glycosylation LOCATION: 152 to 154 LIDENTIFICATION METHOD: similarity with known IDENTIFICATION METHOD: sequence NAME/KEY: N-linked glycosylation LOCATION: 177 to 179 IDEWILFICATION METHOD: similarity with known IDENITFICATION METHOD: sequence IDENTIFICATION METHOD: similarity with known IDENTIFICATION METHOD: sequence NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
LDENTIFICATION METHOD: similarity with known
LDENTIFICATION METHOD: sequence IDENTIFICATION METHOD: similarity with known IDENTIFICATION METHOD: sequence NAME/KEY: N-linked glycosylation LOCATION: 173 to 175 IDENTIFICATION METHOD: similarity with known BENTIFICATION METHOD: sequence similarity with known IDENTIFICATION METHOD: soluble protein OTHER INFORMATION: hydrophobic NAME/KEY: N-linked glycosylation LOCATION: 19 to 21 NAME/KEY: N-linked glycosylation LOCATION: 192 to 194 IDENTIFICATION METHOD: similarit: IDENTIFICATION METHOD: sequence NAME/KEY: N-linked glycosylation LOCATION: 64 to 66 sedneuce NAME/KEY: transmembrane domain NAME/KEY: extracellular domain FREEMAN, GORDON J. FREEDMAN, ARNOLD S. SEGIL, JEFFREY M. LEE, GRACE WHITMAN, JAMES F. NAME/KEY: Ig V-set domain LOCATION: 1 to 104 AUTHORS: AUTHORS: AUTHORS: AUTHORS:

61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTIVSQDPETELYAVSSKLDF 180 Gaps 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKWVLTMMSGDMNIWPE 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSKLDF AUTHORS: NADLER, LEE M. TITLE: B7, A New Member Of The Ig Superfamily With TITLE: Unique Expression On Activated And Neoplastic B Cells JOURRAL: The Journal of Immunology VOLUME: 143 ö US-08-479-744A-29
Sequence 29, Application US/08479744A
Sequence 29, Application US/08479744A
Sequence 29, Application US/08479744A
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street Length 288; Indels PAGES: 2714-2722 DATE: 15-OCT-1989 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPRATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: June 7, 1995
CLASSIFICATION: 435 Ouery Match 100.0%; Score 1149; DB 3; Best Local Similarity 100.0%; Pred. No. 5.5e-113; Matches 216; Conservative 0; Mismatches 0; 181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242 NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624 FILING DATE: 26-JULY-1993 APPLICATION NUMBER: 08/147,773 FILING DATE: 3-NOV-1993 ATTORNEY/AGENT INFORMATION: Massachusetts USA COUNTRY: US US-08-153-262-2 ISSUE: PAGES: STATE: RESULT 6 g οy g ŏλ Ω δλ

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MOLECULE TYPE: protein DESCRIPTION: B cell activation antigen; natural ligand DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
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LOCATION: -34 to -1
LOENTIFICATION METHOD: amino terminal sequencing
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
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LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
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LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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LOCATION: 55 to 57
LOCATION: 55 to 57
SERVILEICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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LOCATION: 152 to 154
LOENTICON: 152 to 164
SIENTIFICATION METHOD: SEQUENCE
IDENTIFICATION METHOD: SEQUENCE
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LOCATION: 173 to 175
ENENTERICATION METHOD: Similarity with known
IDENTIFICATION METHOD: Sequence
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LOCATION: 192 to 194
BENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity
IDENTIFICATION METHOD: sequence
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LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity
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TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
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                                                                                                                                                                       linear
                                                                                                                                                                    TOPOLOGY:
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61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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                                                                                                                                                                  PUBLICATION INFORMATION:
AUTHORS: FREEDAM, GORDON J.
AUTHORS: SECIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262 US-08-479-744A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/280,757B
FILING DATE: 26-JUL-1994
               IDENTIFICATION METHOD: similarity with known IDENTIFICATION METHOD: sequence
                                                                                 NAME/KEY: Ig C-set domain
LOCATION: 105 to 20
LOCATION: 105 to 20
LOCATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NMTINHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Journal of Immunology
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Fatent No. 6130316
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Gray, Gary S.
APPLICANT: Greenfield, Edward
TITLE OF INVENTION: No. 6130316el CT.
TITLE OF INVENTION: Uses Therefor
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CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 100.0
Matches 216; Conservative
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STATE: Massachusetts
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
LOCATION: 1 to 104
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15-0CT-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein DESCRIPTION: B cell activation antigen; natural ligand DESCRIPTION: Cor CD28 T cell surface antigen; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of IDENTIFICATION METHOD: soluble protein OTHER INFORMATION: hydrophobic
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LOCATION: 173 to 175
LEBUTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
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LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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LOCATION: 152 to 154
IDEWILFICATION METHOD: similarity with known
IDENITFICATION METHOD: sequence
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LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MANDER: AMPLEANT OF THE CONTROL OF THE CONTRO
                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/109,393
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: N-linked glycosylation LOCATION: 19 to 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: intracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: signal sequence LOCATION: -34 to -1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 209 to 235
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
CLASSIFICATION: 435
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61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-09-135-2
i Sequence 2, Application US/09159135
sequenc
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B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
The Journal of Immunology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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; RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262
US-08-280-7578-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1149; DB 4;
100.0%; Pred. No. 5.5e-113;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
LOCATION: 105 to 202
LOCATION HORY STATE AND AND TOWN TELEGRATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
                                                                                                                                                                                                                                                                                                              NAME/KEY: N-linked glycosylation
LOCATION: 198 to 20
ENERTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD: similarity with known IDENTIFICATION METHOD: sequence
                                                                                                                                                                          similarity with known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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                                                                                     NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEGIL, JEFFREY M.
LEE, GRACE
WHITMAN, JAMES F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Ig V-set domain LOCATION: 1 to 104
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Best Local Similarity 100.
Matches 216; Conservative
IDENTIFICATION METHOD:
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VOLUME: 1
ISSUE: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS:
AUTHORS:
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VOLUME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein DESCRIPTION: B cell activation antigen; natural ligand DESCRIPTION: Cor CD28 T cell surface antigen; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity with known sequence
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IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
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LOCATION: 152 to 154
IDENTIFICATION METHOD: Similarity
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: N-linked glycosylation LOCATION: 64 to 66
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APPLICATION NUMBER: 08/147,772
FILING DATE:
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LOCATION: 209 tO 235
IDENTIFICATION METHOD: sequence
IDENTIFICATION METHOD: sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: intracellular domain
                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                        STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                               COUNTRY:
ZIP: 0210
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61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 1149; DB 4; Length 288; Best Local Similarity 100.0%; Pred. No. 5.5e-113; Matches 216; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2: From -26 to 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: IG C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
                                                                                                                               NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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                                                       similarity with known
                                                                                                                                                                                                                                                                                                           similarity with known sequence
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NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: Similarity
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                        NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: Similarity
IDENTIFICATION METHOD: sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ISSUE: 8
; PAGES: 2714-2722
DATE: 15-OCT-1989
; RELEVAMY RESIDUES IN SEQ ID NO:
US-09-159-135-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS: FREEDMAN, ARNOLD S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: IG V-set domain LOCATION: 1 to 104
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US-08-205-697A-19
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APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon J.
APPLICANT: Wadler, Lee M.
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
CORRESPONDENCES: 61
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKWVLTMMSGDMNIWPE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1149; DB 4; Length 288; Best Local Similarity 100.0%; Pred. No. 5.5e-113; Matches 216; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205,697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                      E: LAHIVE & COCKFIELD
60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFRENCE/DOCKET NUMBER: BMI-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 288 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                        Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                   STATE: Mar
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                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-08-702-525-19
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147 ISDFEIPTSNIRRIICSTSGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSKLDF 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Balmcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Nadler, Lee M.
APPLICANT: Nadler, Lee M.
APPLICANT: Nadler, Lee M.
APPLICANT: ACOURNES: 4
CORRESPONDENCE ADDRESS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1149; DB 4; Length 288; Best Local Similarity 100.0%; Pred. No. 5.5e-113; Matches 216; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 NMTINHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
                                                                                                                                                                                                                                                                                                                                              NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120CPUS
TELECOMMUNICATION INFORMATION:
TELEPAHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: LAHIVE & COCKFIELD 60 State Street, Suite 510
                                                                                                       COMPUTER: IN TOTAL COMPATIBLE COMPUTER: DAYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/702,525
                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-450-798-2; Sequence 2, Application US/09450798; Patent No. 6319709; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 288 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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STATE: Massachusetts
Massachusetts
                                                                  COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy
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                                       02109-1875
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                                                                                                                                                                                                                                    FILING DATE:
                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02109
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                   COUNTRY:
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APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
APPLICANT: Gray, Gary S., Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cell
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE: Unique Expression On Activated And Neoplastic B Cells JOURNAL: The Journal of Immunology VOLUME: 143
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100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE: B7, A New Member Of The Ig Superfamily With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
                                                     NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
ENERITEICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                       LOCATION: 198 to 200 IDENTIFICATION METHOD: similarity with known IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD: similarity with known IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Ig C-set domain
LOCATION: 105 to 20
LOCATION: 105 to 20
LOCATION METHOD: Similarity with known
IDENTIFICATION METHOD: sequence
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                                                                                                                                                                                           NAME/KEY: N-linked glycosylation
        sednence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBLICATION INFORMATION:
AUTHORS: FREEDAMN, GORDON J.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
                                                                                                                                                                                                                                                                                                                                NAME/KEY: IG V-set domain LOCATION: 1 to 104
     IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-403-253A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/450,798
FILING DATE: 29-NOV-1999
PRIOR APPLICATION NUMBER: US/08/147,772
FILING DATE: 03-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36.207
REFERENCE/POCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acids
TYPE: Amino acids
TYPE: ACCUMENT INFORMATION:
TOTAL TABLET THERETORY
TYPE: Amino acids
TYPE: Amino acids
TYPE: ACCUMENT THERETORY
TOTAL THERETORY
TOTAL THERETORY
TYPE: Amino acids
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LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
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IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
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LOCATION: 152 to 154
EMENTELCATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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sequence
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LOCATION: 19 to 21
IDENTIFICATION METHOD: similarit:
IDENTIFICATION METHOD: sequence
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LOCATION: 64 to 66
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OPERATING SYSTEM: PC-DOS/MS-DOS
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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NADLER, LEE M.
B7, New Member of The Ig Superfamily With
B7, A New Expression on Activated And Neoplastic B Cells
The Journal of Immunology
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; RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-403-253A-2
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LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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LOCATION: 105 to 202
IDENTIFICATION METHOD: Similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 198 to 200 similarity with known IDENTIFICATION METHOD: sequence
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
EDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 173 to 175 interpretation of the control 
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LOCATION: 177 to 179
IDENTIFICATION METHOD: similarit:
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity
IDENTIFICATION METHOD: sequence
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LOCATION: 173 to 175
                                                                                                                                                                                N-linked glycosylation
64 to 66
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FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
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Best Local Similarity 100.
Matches 216; Conservative
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                                                                                                                                                                                    NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
                                                                                                                                                                             SOFTWARES: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,253A
FILING DATE: March 10, 1995
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US 08/253,964
APPLICATION NUMBER: US 08/253,964
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: transmembrane domain
LOCATION: 209 to 235
LIDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP2
TELECOMNUNICATION INFORMATION:
TELEPANE: (617) 227-7400
ITELEPANE: (617) 742-4214
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 16 UNE 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 UNE 1992
APPLICATION NUMBER: US 07/7975,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247 FAILING NAME: US 08/247 FAILING NAME: US 08/247 FAILING NAME: US 08/247 FAILING NAME: US 08/247 FAILING NAME:
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LOCATION: 19 to 21
                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: hydrophobic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 amino acids
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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                  ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                                                                                                                                                           APPLICANT: Green et al
TITLE OF INVENTION: Polynuclectides Encoding Members of the Human B
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 15965-562 (CURA-62)
CURRENT APPLICATION NUMBER: 060/152383
FRIOR APPLICATION NUMBER: 60/152383
FRIOR APPLICATION NUMBER: 60/172909
FRIOR APPLICATION NUMBER: 60/172909
FRIOR PILING DATE: 1999-12-21
FRIOR FILING DATE: 1999-12-21
FRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules TITLE OF INVENTION: and Uses Therefor NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 288;
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Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0;
                                                                           181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                   207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application PC/TUS9502576 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                               US-09-651-200-13; Sequence 13, Application US/09651200; Patent No. 6429303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS: ADDRESSEE: LAHIVE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens US-09-651-200-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Green et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US95-02576-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 13
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APPLICANT: Emery, Stephen
APPLICANT: Copley, Clive Graham
APPLICANT: Copley, Clive Graham
APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/17,945
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR PELING DATE: 1996-05-04
PRIOR PELING DATE: 1996-05-04
PRIOR FILING DATE: 1997-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: humanized
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Length 288;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1149; DB 5;
100.0%; Pred. No. 5.5e-113;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                 NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REPERBNOE/DOCKET NUMBER: BMI-120CPPC
TELECOMMUNICATION INFORMATION:
TELEFAX: (617)227-7400
FELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02576
                                                                                                                                                       FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 131, Application US/09171945; Patent No. 6277599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 100.0
Matches 216; Conservative
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MOLECULE TYPE: protein
PCT-US95-02576-19
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US-09-171-945-131
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Search completed: January 6, 2003, 14:25:51 Job time : 16 secs

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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: January 6, 2003, 14:25:11; Search time 11 Seconds

(without alignments)
372.139 Million cell updates/sec

Title: US-09-454-651B-23
Perfect score: 1499-454-651B-23
Sequence: 1GLSHFCSGVIHVTKEVKEVA......LRVNOTFNWNTTKQEHFPDN 216
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Published_Applications_AA:*

1. /cgn2_6/ptodatta/2/pubpaa/USOB_NEW_PUB.pep:*
2. /cgn2_6/ptodatta/2/pubpaa/PCT_WINE_DUB.pep:*
3. /cgn2_6/ptodatta/2/pubpaa/PCT_WINE_DUB.pep:*
4. /cgn2_6/ptodatta/2/pubpaa/USO6_NEW_PUB.pep:*
5. /cgn2_6/ptodatta/2/pubpaa/USO6_PUBCOMB.pep:*
6. /cgn2_6/ptodatta/2/pubpaa/USO7_PUBCOMB.pep:*
7. /cgn2_6/ptodatta/2/pubpaa/USO7_PUBCOMB.pep:*
8. /cgn2_6/ptodatta/2/pubpaa/USO9_PUBCOMB.pep:*
9. /cgn2_6/ptodatta/2/pubpaa/USO9_NEW_PUB.pep:*
10. /cgn2_6/ptodatta/2/pubpaa/USO9_NEW_PUB.pep:*
11: /cgn2_6/ptodatta/2/pubpaa/USO9_NEW_PUB.pep:*
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12: /cgn2_6/ptodatta/2/pubpaa/USO9_NEW_PUB.pep:*
13: /cgn2_6/ptodatta/2/pubpaa/USO9_NEW_PUB.pep:*
14: /cgn2_6/ptodatta/2/pubpaa/USO0_NEW_PUB.pep:*
14: /cgn2_6/ptodatta/2/pubpaa/USO0_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 21, Appl	Sequence 2, Appli		Sequence 15, Appl	Sequence 14, Appl	Sequence 19, Appl	Sequence 5, Appli	Sequence 131, App	Sequence 3, Appli	4	Sequence 15, Appl	C	N	Sequence 4, Appli	Sequence 4, Appli	17,	Sequence 2, Appli	Sequence 9, Appli	Sequence 11, Appl
ID	US-09-915-789A-21	US-08-592-711-2	US-09-896-738-10	US-09-915-789A-15	US-09-772-102-14	US-09-837-867A-19	US-09-910-174A-5	US-09-910-059-131	US-09-845-899A-3	US-09-955-866-4	US-09-756-983-15	US-09-303-510-2	US-09-303-040-2	US-09-303-510-4	US-09-303-040-4	US-09-837-867A-17	US-09-837-867A-2	US-09-837-867A-9	US-09-837-867A-11
% Query Match Length DB	226 9	288 8	288 9	288 9	288 10	288 10	288 10	473 10	492 10	224 10	313 10	292 10	292 10	292 10	292 10	306 10	320 10	200 10	214 10
% Query Match L	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.5	90.7	79.6	64.7	64.7	64.3	64.3	48.8	48.8	27.1	27.1
Score	1149	1149	1149	1149	1149	1149	1149	1149	1143	1042	915	743	743	739	739	561	561	311	311
Result No.	7	7	3	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19

Sequence 6, Appli	Sequence 6, Appli	Sequence 22, Appl	Sequence 5, Appli	Sequence 11, Appl	Sequence 16, Appl	Sequence 5, Appli	Seguence 6, Appli	Sequence 4, Appli	Sequence 23, Appl	Sequence 18, Appl	Sequence 13, Appl	Sequence 136, App	Seguence 7, Appli	Sequence 7, Appli	Sequence 812, App	Sequence 11, Appl	Sequence 18, Appl	Seguence 630, App	Sequence 810, App	Sequence 5, Appli	Sequence 23, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 12, Appl
US-09-303-510-6	US-09-303-040-6		US-09-845-899A-5				US-09-910-174A-6	ט	US-09-837-867A-23		US-09-896-738-13	US-09-789-561-136	US-09-955-866-7			_	D	US-09-764-853-630			_	us-10-068-215-2		US-10-068-215-4	US-09-896-913A-12
10	10	6	10	σ	6	10	10	æ	10	10	σ	10	10	10	10	σ	σ	10	10	10	6	δ	12	6	6
329	329	219	260	323	323	323	324	329	329	351	302	302	302	309	344	241	302	343	345	480	220	245	245	290	290
17.4	17.4	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	14.0	14.0	•	14.0	14.0	13.9	13.9	13.9	13.9	13.8	13.6	13.6	13.6	13.6	13.6
200.5	200.5	182	182	182	182	182	182	182	182	182	161	161	161	161	161	160	160	160	160	158.5	156.5	156.5	156.5	156.5	156.5
20	21	22	23	24	25	36	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	°,				
	Gaps	09	120	180	
		WPE 	TPS TPS	LDF - LDF	
	26; 0;	GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 	YKNRTIEDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 	ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELMAINTTVSQDPETELTAVSSKLDF 	
ОКУ	th ?	MMSC - - MMSC	LSVI	ELYI 	
ULAT	Length 226; Indels 0	MVE1	AEVT	OPET OPET	
OREG	6,60	KEKK 	REHI 	TVSC	
MMUN	DB 9; 4e-86; 0;	IYWC	DAFK DAFK	AINT	216 226
EL I	Score 1149; DB 9; Pred. No. 3.4e-86; 0; Mismatches 0;	AQTR AQTR	KYEK KYEK	EELN EELN	PDN PDN
NOV 5,78 991	e 11 . No smat	VEEL VEEL	CAAF	LENG ENG	QEHE QEHE
789A -H4, 9/91 220,	Score 1149; Pred. No. 3. Mismatches	HNVS	STYE STYE	HLSW HLSW	NWTTNISEMCLIKYGHLRVNQTENMYTKQEHFPDN
99157 SS SS SS SS O4 (1976)	o,	LSCG] LSCG] LSCG]	PSDE(FPEP	FFNW
15/05 1 ANI 2 CULL 2 COLL 2 COLL 2 COLL 2 COLL 2 COLL 2 COLL 2 COLL 2 COLL 2 COLL 2 COLL 3 COLL 4 ANI 6 COLL 6 COLL 7 COLL 7 COLL 7 COLL 7 COLL 7 COLL 7 COLL 7 COLL 8 COLL 7 COLL 8	100.0%; 100.0%; ive	SVATI	ALRI	1866] 866]	SVNQ - - SVNQ
on U 62A1 62A1 11 H3 77 - H3 MOLE 12 15 17 - H3 17 - H3 17 - H3 18 - H	10 10 rativ	EVKI - - (EVKI	IVII 		GHLI GHLI GHLI
ication 0168762 0168762 0168762 0018 0018 001 07039-2 07039-2 07039-2 07039-2 07039-2 07039-2 07039-2 07039-2 0705-2 0705-2 0705-2 0705-2	ity serv	HVT.	NNLS	IRRI IIRRI	
1 0020 0020 0020 0020 en, 0020 CATI C DA TATON TATON TATON	ilar Con	SGVI SGVI	FDIT FDIT	PTSN 	SFMC SFMC
JA-2 1, A-2 1, A-2 10S2 10S2 10NVE 11LIN 11LIN 11CA 11CA 11CA 11CA 11CA 11CA 11CA 11C	h Sim 16;	SHEC	NRTI 	DFEI DFEI	TTNH
S-78 NO. CANT OF OF NO. REFE REFE ROF ROF ROF ROF ROF ROF ROF ROF ROF ROF	Matc. ocal				
RESULT 1 Sequence 21, Application US/09915789A Sequence 21, Application US/09915789A Patent No. US20020168762A1 GENERAL INFORMATION: APPLICANT: Chen, Lieping TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY TITLE OF INVENTION: MOLECULES FILE REFERENCE: 07039-219001 CURRENT PEPLICATION NUMBER: US/09/915,789A CURRENT FILING DATE: 2000-06-04 PRIOR PRICA ELON NUMBER: US 60/220,991 PRIOR FILING DATE: 2000-07-27 NUMBER OF SEQ ID NOS: 23 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 21 LENGTH: 226 TYPE: PRT ORGANISM: Homo sapiens US-09-915-789A-21	Query Match Best Local Similarity 100 Matches 216; Conservative	11	61	121	181
RESULT Seque Seque Seque APP TIT FILL FILL FILL PRI PRI SOUR SOUR SOO SOO SOO SOO SOO SOO SOO SOO SOO SO	Que Bes Mat	QY Dp	Oy Dp	Qy	Qy
MD WWWWWWWWWWWWWWWWWWWWWW		٠	У I	> 1	<u> </u>

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AUTHORS: LEE, GRACE
AUTHORS: WHITHANN, DAMES F.
AUTHORS: NADLER, LEE M.
IITLE: B7, A New Member Of The Ig Superfamily With
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LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
                                                      LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                     LOCATION: 209 to 235
IDENTIFICATION METHOD: Similarity with known
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
LIBENTEICATION METHOD: Similarity with known
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION METHOD: similarity with known IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD: similarity with known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity with known
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LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
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LOCATION: 1 to 104
LEBUTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                            similarity with known
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: N-linked glycosylation LOCATION: 55 to 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: Similarity
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarit;
IDENTIFICATION METHOD: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: N-linked glycosylation
LOCATYON: 177 to 179
LIBRITEICATION METHOD: similarity
IDENTIFICATION METHOD: sequence
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LOCATION: 192 to 194
IDENTIFICATION METHOD: similarit;
IDENTIFICATION METHOD: sequence
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                                   extracellular domain
                                                                                                                                                                  transmembrane domain
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FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
                                                                                                                                                                                                                                                                                                                    LOCATION: 236 to 254
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD: FEATURE:
                                                                                                                                    FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                            APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary J.
APPLICANT: Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: -34 to -1.
IDENTIFICATION METHOD: amino terminal sequencing of IDENTIFICATION METHOD: soluble protein OTHER INFORMATION: hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEN PC Compatible
COMPUTER: PEN PC COMPATIBLE
COMPUTER: PATENTINE PC-DOS/MS-DOS
SOFTWARE: PATENTINE POSTORS #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,711
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,816
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3-UUNE-1994
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3-UUNE-1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3-UUNE-1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3-UUNE-1994
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/864,866 FILING DATE: 7-APR-1992 APPLICATION NUMBER: US 08/218,155 FILING DATE: 25-MAR-1994 APPLICATION NUMBER: US 07/864,807 FILING DATE: 7-APR-1992 APPLICATION NUMBER: US 07/902,467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOOKET NUMBER: RPI-002CP4
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/247,505 FILING DATE: 23-MAY-1994
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APPLICATION NUMBER: US 07/275,433
FILING DATE: 23-NOV-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                      Sequence 2, Application US/08592711
Patent No. US20020115214A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: signal sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 23-MAY APPLICATION NUMBER: FILING DATE: 7-APR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                         GENERAL INFORMATION:
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STREET: bv
-mv: Boston
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RESULT 2
US-08-592-711-2
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                                                                                                                                                                                                                                                                                                                                                      61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                         1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
Unique Expression On Activated And Neoplastic B Cells: The Journal of Immunology
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Patent No. US20020165347A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL PROPERTY SULIVAN, John K.
APPLICANT: Sullivan, John K.
APPLICANT: Fang, Mei
TITLE OF INVENTION: 37-Like Molecules and Uses Thereof
FILE REFERENCE: 00-513-A
CURRENT APPLICATION NUMBER: US/09/896,738
CURRENT FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
                                                                                                                   2: From -26 to 262
                                                                                                                                                                          100.0%; Score 1149; DB 8;
illarity 100.0%; Pred. No. 4.5e-86;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match' 100.0%; Score 1149; DB 9;
Best Local Similarity 100.0%; Pred. No. 4.5e-86;
Matches 216; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                   ; RELEVANT RESIDUES IN SEQ ID NO: US-08-592-711-2
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SOFWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens US-09-896-738-10
                                                                                               15-0CT-1989
                                                                             2714-2722
                                                                                                                                                                                            Best Local Similarity
Matches 216; Conserv
                    JOURNAL: The VOLUME: 143
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US-09-896-738-10
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                                                                               PAGES:
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61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 100.0%; Score 1149; DB 9; Length 288; Best Local Similarity 100.0%; Pred. No. 4.5e-86; Matches 216; Conservative 0; Mismatches 0; Indels 0
                                                                                                       APPLICANT: Chen, Lieping
TITLE OF INVENTION:
TITLE OF INVENTION:
MOLECULES
FILE REPERENCE: 07039-219001
CURRENT PELLING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 60/220,991
PRIOR PELLING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09772102

Patent No. US20020006413A1

GENERAL INFORMATION:

APPLICANT: Shawler, Daniel L.

APPLICANT: Shawler, Daniel L.

APPLICANT: Bartholomew, Richard M.

APPLICANT: Gold, Daniel P.

TITLE OF INVENTION: Genetically Engineered Tumor Cell

TITLE OF INVENTION: Waccines

FILE OF INVENTION NUMBER: US 60/172,102

CURRENT FILING DATE: 2000-01-26

PRIOR FILING DATE: 2000-01-27

PRIOR FILING DATE: 2000-01-27
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100.0%; Pred. No. 4.5e-86;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 14 LENGTH: 288
                                                      Sequence 15, Application US/09915789A Patent No. US20020168762A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 216; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-915-789A-15
RESULT 4
US-09-915-789A-15
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US-09-772-102-14
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LENGTH: 288
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Gaps

Indels

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APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. US20020106730Alel Members of the B7
TITLE OF INVENTION: Family and Uses Thereof
FILE REFERENCE: 35800/236924
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                                                                                                           61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                           121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                                                                                       APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaulo
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Godon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. US20020098542Alel Forms of T Cell Costimulatory
TITLE OF INVENTION: Molecules and Uses Therefor
FILE REFERENCE: BWI-120CPADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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                                                                                                                                                                                                                                                                181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                         207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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PRIOR APPLICATION NUMBER: 08/205,697
PRIOR FILING DATE: 1994-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 216; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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US-09-837-867A-19
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Sequence 131, Application US/09910059

Patent No. US20020142359A1

GENERAL INDORMATION:

APPLICANT: Copley, Clive G

APPLICANT: Edge, Michael Derek

TITLE OF INVENTION: Their Therapeutic use in an Adept System

FILE REFERENCE: 1991-209

CURRENT FILING DATE: 1998-10-229

PRIOR FILING DATE: 1997-04-29

PRIOR FILING DATE: 1997-04-29

PRIOR FILING DATE: 1997-02-14

PRIOR FILING DATE: 1997-02-14

PRIOR FILING DATE: 1996-05-04

PRIOR FILING DATE: 1996-05-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                               27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE
                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                               Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: full-length human B7.1-murine ASB7 Fd fusion US-09-910-059-131
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                                                                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.5e-86;
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100.0%; Pred. No. 8.2e-86;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                            100.0%; Score 1149; 100.0%; Pred. No. 4.
CURRENT APPLICATION NUMBER: US/09/910,174A
CURRENT FILING DATE: 2001.07-20
PRIOR APPLICATION NUMBER: US 09/620,461
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Matches 216; Conservative
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                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                  LENGTH: 288
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                                                                                                                                                                                                                                                                                                                  Query Match
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                                                        ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF
                                                                                             147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF
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GENERAL INCORMATION:
APPLICANT: CHAIKIN, MARGERY ANN
APPLICANT: TIN, SALLY DORREN PATRICIA
APPLICANT: WIEST, RAYMOND W.
APPLICANT: TRUBET, RAYMOND W.
TITLE OF INVENTION: HEXAMERIC FUSION PROTEINS AND USES;
TITLE OF INVENTION: HEXAMERIC FUSION PROTEINS AND USES;
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: P50496
CURRENT FILING DATE: 2001-04-30
PRIOR FILING DATE: 1999-01-13
PRIOR APPLICATION NUMBER: US 60/043,948
PRIOR FILING DATE: 1997-02-19
PRIOR FILING DATE: 1997-02-19
PRIOR FILING DATE: 1997-02-13
PRIOR FILING DATE: 1997-02-13
SEO ID NOS: 27
SEO ID NOS: 27
LENGTH: 492
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APPLICANT: Fox, Michael
APPLICANT: Sullivan, John K.
APPLICANT: Holst, Paige
APPLICANT: Holst, Paige
APPLICANT: Town Might Steven Kiyoshi
TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof
FILE REFERENCE: 00,759-A
CURRENT APPLICATION NUMBER: US/09/955,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.5%; Score 1143; DB 10;
100.0%; Pred. No. 2.6e-85;
iive 0; Mismatches 0;
                                                                                                                                     NMTINHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                         NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPD 215
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Matches 215; Conservative
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                                                                                                                                                                                                                                                         US-09-845-899A-3
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TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS.
TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS.
TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS.
CURRENT APPLICATION NUMBER: US/09/756,983
CURRENT FILING DATE: 1998-10-19
PRIOR FILING DATE: 1998-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 15
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100.0%; Pred. No. 4.3e-67;
tive 0; Mismatches 0;
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              PRIOR APPLICATION NUMBER: 60/233,867 PRIOR FILING DATE: 2000-09-20 NUMBER OF SEQ ID NOS: 30 SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2001-09-19
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Matches 175; Conservative
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                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-955-866-4
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Best Local Similarity
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                                                                                                                                 LENGTH: 224
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                                                                                                              SEQ ID NO 4
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208 MTNNHSFLCLVKYGNLLVSQIFNWQ--KSEPQPSN 240
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        33; Mismatches
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CURRENT FILING DATE: 1999-04-30
EARLIER APPLICATION NUMBER: 60/083,869
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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      Matches 136; Conservative
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ORGANISM: Feline
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US-09-303-510-4
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APPLICANT: COCTAIN, Mark D.
TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
TITLE OF INVENTION: Feline CD80, Feline CD28, Feline CTLA-4 or
TITLE OF INVENTION: Feline Interferon-gama And Uses Thereof
FILE REFERENCE: 54957-B
CURRENT APPLICATION NUMBER: US/09/303,040
CURRENT FILING DATE: 1999-04-30
EARLIER FILING DATE: 1999-05-01
NUMBER OF SEQ ID NOS: 82
                                                                                                               Sequence 2, Application US/09303510A
Patent No. US20020028208A1
GENERAL INFORMATION:
APPLICANT: Collisson, Ellen W.
APPLICANT: Choi, InSoo
TITLE OF INVENTION: Feline CD86, Feline CD28, and Feline
TITLE OF INVENTION: CLA-4 Nucleic Acid and Polypeptides
TILE REFERENCE: 54954
CURRENT APPLICATION NUMBER: US/09/303,510A
CURRENT FILING DATE: 1999-04-30
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 83
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63.38;
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Matches 136; Conservative
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ORGANISM: feline CD80
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Best Local Similarity
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T.F.NGTH: 292
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US-09-303-040-2
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APPLICANT: Winslow, Barbara J.
TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
TITLE OF INVENTION: Reline CB80, Feline CD88, Feline CTLA-4 or
TITLE OF INVENTION: Feline Interferon-gama And Uses Thereof
                                                                                                                                                                                                            62 KNRTIFDITUNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
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                                                                                          28 LFYFCSGIIQVNKTVEEVAVLSCDYNISTKELTEIRIXWQKDDEMVLAVMSGKVQVWPKY 87
                                                       2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
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Sequence 4. Application US/09303510A

Patent No. US20020028208A1

GENERAL INFORMATION:
APPLICANT: Collisson, Ellen W.
APPLICANT: Hash, Stephen M.
APPLICANT: How, InSoo
TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline
TITLE OF INVENTION: CTLA-4 Nucleic Acid and Polypeptides
FILE REFERENCE: 54954
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44; Indels
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64.3%; Score 739; DB 10; Length 292;
Best Local Similarity 62.8%; Pred. No. 7e-53;
Matches 135; Conservative 34; Mismatches 44; Indels
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CURRENT APPLICATION NUMBER: US/09/303,040
CURRENT FILING DATE: 1999-04-30
EARLIER APPLICATION NUMBER: 60/083,870
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 292
TYPE: PRT
TYPE: PRT
USGANISM: feline CD80
US-09-303-040-4
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein January 6, 2003, 14:24:10 ; Search time 143 Seconds Run on:

(without alignments) 973.863 Million cell updates/sec

Title:

US-09-454-651B-23 1149 1 GLSHFCSGVIHVTKEVKEVA......LRVNQTFNWNTTKQEHFPDN 216 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

4569144 seqs, 644733110 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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(cgn2_6/ptodate/1/paa/US06_COMB.pep:*
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(cgn2_6/ptodate/1/paa/US081_COMB.pep:*
(cgn2_6/ptodate/1/paa/US081_COMB.pep:*
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(cgn2_6/ptodate/1/paa/US096_COMB.pep:* Pending_Patents_AA_Main:*
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/cgn2_6/ptodata/1/paa/US098_COMB.pep:/cgn2_6/ptodata/1/paa/US099_COMB.pep:/cgn2_6/ptodata/1/paa/US100_COMB.pep:/cgn2_6/ptodata/1/paa/US101_COMB.pep:/cgn2_6/ptodata/1/paa/US101_COMB.pep:/cgn2_6/ptodata/1/paa/US102_COMB.pep: /cgn2_6/ptodata/1/paa/US095_COMB.pep:* /cgn2_6/ptodata/1/paa/US096_COMB.pep:* /cgn2_6/ptodata/1/paa/US097_COMB.pep:* /cgn2_6/ptodata/1/paa/US60_COMB.pep:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 8, Appli					
SUMMARIES		ID	8 US-08-459-766B-8	US-09-454-651B-23	US-09-569-164A-8	PCT-US01-41430-21	US-09-915-789A-21	PCT-US01-06769-12
		DB	: &	18	19	Н	23	
		Length	216	216	216	226	226	248
	дP	Query re Match Length DB ID	100.0	100.0	100.0	100.0	100.0	100.0
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1 PCT-US01-41430- 1 PCT-US02-09671- 1 PCT-US02-09671-	1 PCT -USO2 -09671 -196 1 PCT -USO2 -09671 -197 2 US -08 -109 -393A -29 5 US -08 -109 -393A -29 6 US -08 -280 -57 -29 8 US -08 -435 -816A -2	8 US-08-453-386-2 9 US-08-53-318-5-2 15 US-09-183-055-1 16 US-09-206-1132-1 17 US-09-349-915A 17 US-09-349-915A 17 US-09-349-915A 17 US-09-349-915A 17 US-09-349-915A 18 US-09-425-516-1 19 US-09-522-2068 19 US-09-522-2068 19 US-09-523-865-1 19 US-09-553-865-1 19 US-09-553-865-1 19 US-09-553-865-1 19 US-09-553-865-1 19 US-09-553-865-1
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ALIGNMENTS

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liasley, Peter S.
APPLICANT: Ladbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Damle, Nitin K.
TITLE OF INVENTION: LIGAND FOR CD28 RECEPTOR ON B CELLS AND METHODS
TITLE OF INVENTION: LIGAND FOR CD28 RECEPTOR ON B CELLS AND METHODS
FILE REFERENCE: 30436.110S04
CURRENT FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 07/498,949
PRIOR APPLICATION NUMBER: 07/4980
PRIOR FILING DATE: 1990-03-26
PRIOR FILING DATE: 1990-07-02
PRIOR FILING DATE: 1991-06-27
PRIOR FILING DATE: 1991-06-27
PRIOR FILING DATE: 1994-03-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
LENTH: 216
                                               Sequence 8, Application US/08459766B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS: Freeman, Gordon J. AUTHORS: Freedman, Arnold S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens PUBLICATION INFORMATION:
RESULT 1
US-08-459-766B-8
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                                                                                                                                                                                                                                                                                              100.0%; Score 1149; DB 8; Length 216; 100.0%; Pred. No. 8.3e-112; tive 0; Mismatches 0; Indels 0
               AUTHORS: Lee, drace Author James F. AUTHORS: Maller James F. AUTHORS: Maller, Lee M. TITLE: B7, A NEW MEMBER OF THE IG SUPERFAMILY WITH UNIQUE JITLE: SPRESSION ON ACTIVATED AND NEOPLASTIC B CELLS JOURNAL: J. Immunol.
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Damle, Nitin K.
Brady, William
Wallace, Philip M.
TITLE OF INVENTION: CTLA4/CD281g HYBRID FUSION
PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 35 N. Arroyo Parkway, Suite 60
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APPLICATION NUMBER: US/09/454,651B
FILING DATE: 06-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/228,208
FILING DATE: 15-APR-1994
APPLICATION NUMBER: 08/008,898
FILING DATE: 22-JAN-1993
APPLICATION NUMBER: 07/723,617
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B
REGISTRATION NUMBER: 34,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Mandel & Adriano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/09454651B GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
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COMPUTER READABLE FORM: MEDIUM TYPE: Diske
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                                                                                                                                                                                                                                RELEVANT RESIDUES: 1 TO 216
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STATE: California
AUTHORS: Segil, Jeffrey M.
                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
                                                                                                                                                                                      PAGES: 2714-2722
DATE: 1989-10-15
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GENERAL INFORMATION:
TITLE OF INVENTION: LIGAND FOR CD28 RECEPTOR ON B CELLS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1149; DB 18; Length 216; 100.0%; Pred. No. 8.3e-112; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS: Nadler, Lee M. TITLE: B7, A NEW MEMEBER OF THE 19 SUPERFAMILY WITH UNIQUE TITLE: EXPRESSION ON ACTIVATED AND NEOPLASTIC B CELLS
REFERENCE/DOCKET NUMBER: 30436.30USD1
TELECOMUNICATION INFORMATION:
TELEPHONE: 626.395-7801
TELEFAX: 626.395-0694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/569,164A
CURRENT FILIGE DATE: 2000-05-11
PRIOR PILING DATE: 1990-07-02
PRIOR FILING DATE: 1991-07-02
PRIOR FILING DATE: 1991-06-27
PRIOR APPLICATION NUMBER: 07/722,101
PRIOR APPLICATION NUMBER: 08/219,200
PRIOR APPLICATION NUMBER: 08/219,200
PRIOR PILING DATE: 1991-06-27
PRIOR PRILING DATE: 1995-06-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 8
SEQ ID NO 8
                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                          LENGTH: 216 amino acids TYPE: amino acid
                                                                                                                                                                                                     STRANDEDNESS: unknown
                                                                                     TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 23:
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AUTHORS: Freeman, Gordon J.
AUTHORS: Freedman, Arnold S.
AUTHORS: Segil, Jeffrey M.
AUTHORS: Lee, Grace
AUTHORS: Whitman, James F.
                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 100.0
Matches 216; Conservative
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                                                                                                                                                                                                                                                                                                US-09-454-651B-23
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US-09-569-164A-8
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                                                                                                                                  Gaps
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GENERAL INFORMATION:
APPLICANT: MAYO FOUNDATION FOUNDATION:
TITLE OF INVENTION: 97-13 AND 87-44, NOVEL IMMUNOREGULATORY
TITLE OF INVENTION: MOLECULES
FILE REFERENCE: 07039-219W01
CURRENT APPLICATION NUMBER: PCT/US01/41430
CURRENT FILING DATE: 2001-07-26
PRIOR PILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
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0
                                                ; Score 1149; DB 19; Length 216;
; Pred. No. 8.3e-112;
0; Mismatches 0; Indels 0;
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TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
TITLE OF INVENTION: MOLECULES
FILE REFERENCE: 07039-219001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NMT#NHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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                                                100.0%;
RELEVANT RESIDUES: 1 TO 216
                                                                 Best Local Similarity 100.0
Matches 216; Conservative
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LENGTH: 226
                US-09-569-164A-8
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                                                     Query Match
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121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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                                                                                                                                                                                                                                                                        Length 226;
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APPLICANT: Mayo Medical Ventures
TITLE OF INVENTION: hB7-H2, A NOVEL CO-STIMULATORY MOLECULE
FILE REFERENCE: 07039-202001
CURRENT APPLICATION NUMBER: PCT/US01/06769
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/186,519
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
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                                                                                                                                                                                                                                                                      100.0%; Score 1149; DB 23;
100.0%; Pred. No. 8.9e-112;
iive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/915,789A CURRENT FILING DATE: 2002-06-04 PRIOR APPLICATION NUMBER: US 60/220,991 PRIOR FILING DATE: 2000-07-27 SOFTWARE: FASTEQ for Windows Version 4.0
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; GENERAL INFORMATION:
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Matches 216; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 226
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                                                                                       APPLICANT: Mayo Foundation for Medical Education and Research TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY TITLE OF INVENTION: MOLECULES FILE REPERBNCE: 07039-219901
CURRENT APPLICATION NUMBER: PCT/US01/41430
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/220,991
PRIOR APLICATION NUMBER: 60/220,991
PRIOR FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 23
SOFTWARR: PSASEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 288
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GENERAL INFORMATION:
APPLICANT: Zycos Inc.
TITLE OF INVENTION:
FILE REFERENCE: 08191-026W01
CURRENT PAPLICATION NUMBER: PCT/US02/09671
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR APPLICATION NUMBER: 60/299,544
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-06-01
PRIOR PRILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR APPLICATION NUMBER: 60/326,370
PRIOR PILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 60/356,985
PRIOR FILING DATE: 2002-02
NUMBER OF SEQ ID NOS: 2041
SOFTWARE FEASTER FAILNG DATE: 2002-02
RESULT 7
PCT-US01-41430-15
Sequence 15, Application PC/TUS0141430
GENERAL INFORMATION:
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Best Local Similarity 100.C
Matches 216; Conservative
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LENGTH: 288
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61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE
                           27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE
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TITLE OF INVENTION:
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
CURRENT APPLICATION: TRANSLATIONAL PROFILING
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/30,544
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR APPLICATION NUMBER: 60/310,801
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-10-01
PRIOR FILING DATE: 2001-10-01
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR PLING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/336,780
PRIOR APPLICATION NUMBER: 60/336,780
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PRIOR APPLICATION NUMBER: 60/336,780
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SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 288
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147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPFTELYAVSSKLDF 206
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100.0%; Pred. No. 1.3e-111;
tive 0; Mismatches 0;
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TITLE OF INVENTION: TRANSLATIONAL PROFILING FILE REFERENCE: 08191-02601.

CURRENT PELICATION NUMBER: PCT/USO2/09671

CURRENT FILING DATE: 2002-03-28

PRIOR FILING DATE: 2001-03-28

PRIOR FILING DATE: 2001-05-21

PRIOR PRIOR APPLICATION NUMBER: 60/292,544

PRIOR FILING DATE: 2001-05-21

PRIOR FILING DATE: 2001-05-04

PRIOR FILING DATE: 2001-06-08

PRIOR FILING DATE: 2001-06-08

PRIOR FILING DATE: 2001-10-04

PRIOR FILING DATE: 2001-10-04

PRIOR FILING DATE: 2001-10-04

PRIOR FILING DATE: 2001-12-04

PRIOR FILING DATE: 2001-12-04
          TITLE REPERENCE: 08191-026W01
CURRENT APPLICATION NUMBER: PCT/US02/09671
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR PELLING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR PELLING DATE: 2001-05-21
PRIOR PILING DATE: 2001-06-03
PRIOR FILING DATE: 2001-06-03
PRIOR FILING DATE: 2001-06-03
PRIOR FILING DATE: 2001-06-03
PRIOR FILING DATE: 2001-07
PRIOR FILING DATE: 2001-07
PRIOR FILING DATE: 2001-06-03
PRIOR FILING DATE: 2001-07
PRIOR FILING DATE: 2001-07
PRIOR FILING DATE: 2001-07
PRIOR FILING DATE: 2001-07
SPIOR FILING DATE: 2001-07
PRIOR FILING DATE: 2001-07
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 1949
TITLE OF INVENTION: TRANSLATIONAL PROFILING
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Matches 216; Conservative
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PCT-US02-09671-1949
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LENGTH: 288
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                                                                         1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTWMSGDMNIWPE 60
                                                                                                27 GLSHFCSGVIHVITKEVKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIMPE 86
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  Length 288;
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                                      Indels
100.0%; Score 1149; DB 1;
100.0%; Pred. No. 1.3e-111;
ive 0; Mismatches 0;
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TITLE OF INVENTION:
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REBERBENE: 08191-026001
CURRENT APPLICATION NUMBER: PCT/US02/09671
CURRENT FILING DATE: 2002-03-28
PRIOR PELLONION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR PILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR APPLICATION NUMBER: 60/3010,801
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-00-01
PRIOR FILING DATE: 2001-12-04
SPRIOR FILING DATE: 2002-02-20
NUMBER OF SEQ ID NOS: 2041
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 1951
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    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US02-09671-1951
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FILE REFERENCE: 08191-026W01
CURRENT APPLICATION NUMBER: PCT/US02/09671
CURRENT FILING DATE: 2002-03-28
PRIOR PAPLICATION NUMBER: 60/29, 495
PRIOR PELICATION NUMBER: 60/29, 495
PRIOR PELING DATE: 2001-03-28
PRIOR PELING DATE: 2001-05-21
PRIOR PELING DATE: 2001-05-21
PRIOR PAPLICATION NUMBER: 60/30, 801
PRIOR PILING DATE: 2001-09-01
PRIOR PELING DATE: 2001-0-01
PRIOR PELING DATE: 2001-0-1
PRIOR PELING DATE: 2001-10-01
PRIOR PILING DATE: 2001-10-01
PRIOR PELING DATE: 2001-10-01
PRIOR PELING DATE: 2001-12-04
PRIOR PELING DATE: 2001-12-04
PRIOR PELING DATE: 2001-12-04
PRIOR PELING DATE: 2002-02-20
                                                                                                                                    FILE REFERENCETTON NUMBER: PCT/USO2/09671
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/279,495
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-06-08
PRIOR FILING DATE: 2001-10-01
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-20-20
NUMBER OF SEQ ID NOS: 2041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                         Sequence 1952, Application PC/TUS0209671
GENERAL INFORMATION:
APPLICANT: Zyck INC
TITLE OF INVENTION: TRANSLATIONAL PROFILING
FILE REFERENCE: 08191-026W01
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1955, Application PC/TUS0209671 GENERAL INFORMATION:
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PCT-US02-09671-195
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                                                                                                          100.0%; Score 1149; DB 1; Length 288; 100.0%; Pred. No. 1.3e-111;
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TITLE OF INVENTION:
TITLE OF INVENTION:
TRANSLATIONAL PROFILING
FILE REPERENCE: 08191-026M01
CURRENT APPLICATION NUMBER: PCT/US02/09671
CURRENT FILING DATE: 2002-03-28
PRIOR PELING DATE: 2001-03-28
PRIOR PELING DATE: 2001-05-3-1
PRIOR PELING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/292,544
PRIOR FILING DATE: 2001-06-01
PRIOR PELING DATE: 2001-06-01
PRIOR PELING DATE: 2001-06-01
PRIOR FILING DATE: 2001-01
PRIOR FILING DATE: 2001-10-01
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2002-12-04
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SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 1956, Application PC/TUS0209671
; GENERAL INFORMATION:
                                                                                                          Query Match
Best Local Similarity 100.0
Matches 216; Conservative
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                  ; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1955
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ORGANISM: Homo sapiens
PCT-US02-09671-1956
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LENGTH: 288
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Db 207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

Search completed: January 6, 2003, 14:28:21 Job time : 145 secs

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OM protein - protein search, using sw model

January 6, 2003, 14:23:10; Search time 21 Seconds (without alignments) 988.811 Million cell updates/sec Run on:

1149 1 GLSHFCSGVIHVTKEVKEVA......LRVNQTENWNTTKQEHFPDN 216 US-09-454-651B-23 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched: 283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		cell-restricte	B7 protein - red-c			B-lymphocyte activ	spliced	B7-2 antigen - hum		റ.	- human	BARF1 protein - hu	butyrophilin precu	adhesion molecule	surface glycoprote	SHP substrate-1 pr	SHP substrate-1 pr	philin	neural cell adhesi		neural cell adhesi	DM-GRASP precursor		neural cell adhesi	butyrophilin - bov	protein-tyrosine-p	protein-tyrosine k	protein-tyrosine k		hemicentin precurs
£		A45803	G00031	146690	154766	149503	JC7604	A48754	149522	146691	139428	QQBE48	S70587	JH0506	A45254	JC5288	JC5289	S65133	IJXLNL	IJHUNG	JE0099	JH0464	I38049	IJBONC	A37821	TDFFLK	148696	148697	T20992	T43290
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Query	Marci	100.0	94.4	64.2	52.3	48.8	16.1	15.8	13.2	12.2	11.6	11.2		10.7	10.7	10.5			10.1	10.0	9.6	9.6	9.5	9.5	9.5	9.5	9.4	9.4	9.4	9.4
6	acore:	1149	1085	738	601.5	561	185	182	152	140.5	133.5	129	127	122.5	122.5	120.5	120.5	118	116.5	115	112.5	110.5	109.5	109.5	109	109	108	\circ	107.5	107.5
Result		Н	7	٣	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216

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amalgam protein pr neural cell adhesi	neural celebrol be neural celal adhesi Ta kanna chain V r	T-call receptor be T-call receptor be neural cell adhesi	neural cell adhesi	ilbroblast growth neural cell adhesi	neural cell adhesi hypothetical prote	sax-3 protein - Ca SHP substrate-1 pr	neogenin - chicken	cell adhesion prot
A31923 LJRTNC	PLOU64 IJCHNL	RWMSBC	JN0635	A56182 IJMSNG	IJMSNL T29549	T42405	150600	S19247
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333 858	1091	307	1092	480 725	1115	1273	1443	1033
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106.5	105.5	104	104	103.5	103.5	103	102	101
30	3 8 6	5. CJ c	37	38	40	4.4	4 4	45

ALIGNMENTS

	RESULT 1 A45803 B-cell-restricted antigen B7 precursor - human N;Alternate names: B-lymphocyte activation antigen B7
	C;Species: Homo Sapiens (man) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999 C;Accession: IS4495; A45803 p:Selvakumar a : Mchanrai, B.K.; Eddv, R.L.; Shows, T.B.; White, P.C.; Dupont, B.
_	175-181, 1992 Janization and 154495; MUID:9
	A;Accession: I54495 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA
	A;Residues: 1-288 <res> A;Cross-references: GB:M83077; NID:g179327; PIDN:AAA58390.1; PID:g179329 R;Freeman, G.J.; Freedman, A.S.; Segil, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.</res>
	J. Immunol. 183, 2714-2722, 1989 A.Title: B7, a new member of the Ig superfamily with unique expression on activated a A.Title: B7, a new member: A45803; MUID:90010147; PMID:2794510
	A; Accession: A 45 bul 3 A; Molecule type: mRNA A; Residues: 1-288 <frex.< td=""></frex.<>
	A;Cross_references: GB:MZ/533; NID:gl8408U; FIDN:AMAN30U45.1; FID:gsource C;Genetics: A:Cone. Chai.Ch080. Ch088.G1: Ch28
	Ayone: Obs.Coo, Carona, Carona, Ayone: Obs.251792; OMIM:112203 Ayonosition: 3013.3-301.
	A.introns: 34/1; 140/1; 234/1; 266/1 C.Superfamily: B-lymphocyte restricted antigen B7
	C;Keywords: transmembrane protein F;1-26/Domain: signal sequence #status predicted <sig> F;248-264/Domain: transmembrane #status predicted <tmm></tmm></sig>
	Query Match Best Local Similarity 100.0%; Score 1149; DB 2; Length 288; Best Local Similarity 100.0%; Pred. No. 2e-85; Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	QY 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKWYLTMMSGDMNIWPE 60
	61
	Qy 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELXAVSSKLDF 180

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C; Species: Rattus norvegicus (Norway rat)
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 19-May-2000
C; Accession: 154766
R; Judge, T.A.; Liu, M.; Christensen, P.J.; Fak, J.J.; Turka, L.A.
Int. Immunol. 7, 171-178, 1995
A; Title: Cloning the rat homolog of the CD28/CTLA-4-ligand B7-1: structural and funct
A; Reference number: 154766; MUID:9552184; PMID:7537533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Any Strandmark, A. 1993
Any Tile: Genomic organization of the murine B-lymphocyte activation antigen B7.
Any Reference number: 149503; MUID:93307789; PMID:7686531
And Ancession: 149503
Any Status: preliminary; translated from GB/EMBL/DDBJ
And Idecule type: DNA
Anolecule type: DNA
Anolecule type: DNA
Anolecule type: DNA
Anolecule type: DNA
And Anolecule type: DNA
And Anolecule type: DNA
Anolecule type: D
                           149 IGHPDPNVKRIRCSASGGFPEPRLAWMEDGEELNAVNTTVDQDLDTELYSVSSELDFNVT 208
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C;Accession: 149503; S17291; I49521
R;Selvakumar, A.; White, P.C.; Dupont, B.
Immunogenetics 38, 292-295, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U05593; NID:9453381; PIDN:AAA80154.1; PID:9453382 C;Superfamily: B-lymphocyte restricted antigen B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 EYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 SISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GLSHFCSGVI-HVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 52.3%; Score 601.5; DB 2; Best Local Similarity 54.4%; Pred. No. 3.6e-41. Matches 112; Conservative 35; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                  B-lymphocyte activation antigen 7-1 precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                  209 NNHSIVCLIKYGELSVSQIFPWSKPKQE 236
                                                                                                               184 TNHSFMCLIKYGHLRVNQTFNWNTTKQE 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 FNATYDHFIDCFIEYGDAHVSQNFTW 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N; Alternate names: MB7-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-321 <RES>
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C;Date: 14-Peb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
C;Date: 12-Seto, 18-Seto, 18-
                                                                                                                                                                                                                 B7 protein - red-crowned mangabey (fragment)
C;Species: Cercocebus torquatus (red-crowned mangabey, white-collared mangabey)
C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 29-Sep-1999
C;Accession: G00031
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 RTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISD 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 FEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSKLDFNMT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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A;Cross-references: GB:D49843; NID:9755096; PIDN:BAA08643.1; PID:9755097
C;Superfamily: B-lymphocyte restricted antigen B7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A)Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-289 <VIL>
207 NMTINHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242
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                                                                                                                                                                                                                                                                                                                                                                                                 R;Villinger, F.J. submitted to the EMBL Data Library, January 1995
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A; Accession: G00031
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Best Local Similarity
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B7-2 antigen - human
N.Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor
C;Species: Homo sapiens (man)
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A48754; S39055
R;Freeman, G.J.; Gribben, J.G.; Boussiotis, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombar Science 262, 909-911, 1993
A;Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell pr A;Reference number: A48754; MUID:94053735; PMID:7694363
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 02-011-1996 #sequence_revision 02-011-1996 #text_change 23-011-1999
C; Accession: 149522
R; Freeman, G.J; Borriello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kin A; Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell A; Reference number: 149522; MuID:94065585; PMID:7504059
A; Accession: 14952
A; Accession: 14952
A; Molecule type: mRNA
A; Residues: 1-309 < RES>
                                                                                                                                                                                                                                                                                                      A; Status: preliminary
A; Molecule type: mRNBA
A; Molecule type: mRNBA
A; Molecule type: mRNBA
A; Residues: 1-329 CFREA
A; Cross-references: GB:L25259; NID:g416368; PIDN:AAA58389.1; PID:g416369
A; Note: it is uncertain whether Met-1 or Met-7 is the initiator
B; Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza, Mature 366, 76-79, 1993
A; Title: B70 antigen is a second ligand for CTLA-4 and CD28.
A; Reference number: S39055; MUID:94050123; PMID:7694153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 NITENVINITCSSIHGYPEPKKMSVL----LRIKNSTIEYDGIMQKSQDNVTELYDVS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 EVATLSC----GHNVSVEELAQTRIYWQKEKKMVLTMM----SGDMNIWPEYKNRTIFDI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L25606; NID:g432478; PIDN:AAA79770.1; PID:g432479
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:U04343; NID:g439838; PIDN:AAB03814.1; PID:g439839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.8%; Score 182; DB 1; Length 329; 29.0%; Pred. No. 2.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 152; DB 2;
Pred. No. 6.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GDB:433597; OMIM:601020
A;Map position: 3q13.3-3q21
C;Superfamily: B7-2 antigen
C;Keywords: 9lycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 SKLDF---NMTTNHSFMCLIKYGHLRV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 ISLSVSFPDVTSNMTIFCILETDKTRL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%;
26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.8%
Best Local Similarity 29.0%
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: B7-2
C;Superfamily: B7-2 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: CD86; CD28LG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 7-329 <AZU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S39055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Residues: 1-275 <MAG>
C:Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7604
R;Magistrelli, G; Caron, G; Gauchat, J.F.; Jeannin, P.; Bonnefoy, J.Y.; Delneste, Y. Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
A;Title: Identification of an alternatively spliced variant of human CD86 mRNA.
A;Reference number: JC7604; MUID:21092744; PMID:11162656
                                                                                                                                                                                                                                                                                                                                                                                                2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 SDSWTLRTHINLQIKDKGLYQCIIHHKKPTGMIRIHQMNSELSVLANFSQPEI----VPIS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIICSTSGGFPEP-HLSWLENGEELNAINTTV-----SQDPETELYAVS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 KRITCFASGGFPKPRFSWLENGRELPGINTTISQDPESELYTISSQLDFNTTRNHTIKCL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 NLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 RRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNWTTNHSFMCL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GHNVSVEELAQTRIYWQKEKKMVLTMM----SGDMNIWPEYKNRTIFDI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 ETADLPCOFANSONOSLSELV---VFWODOENLVLNEVYLGKEKFDSVHSKYMGRISFD- 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 VTKEVKEVATLSCGHNYSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITN 71
            A;Accession: I49511
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-143,238-274,'R',279-309 <RE2>
A;Cross-references: GB:D16220; NID:g505118; PIDN:BAA03748.1; PID:g994769
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                          Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                       Query Match

48.8%; Score 561; DB 2;
Best Local Similarity 50.7%; Pred. No. 6.5e-38;
Matches 104; Conservative 41; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD86 spliced variant CD86 deltaTM isoform - human
                                                                                                                                                                                                                           A; Cricrons: 37/1; 143/1; 237/1; 275/1
C; Superfamily: B-lymphocyte restricted antigen B7
C; Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 IKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 IKYGDAHVSEDFTWEKPPEDP-PDS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: cd86deltaTM
C;Keywords: immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: nRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: JC7604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 EVATLSC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 SKLDF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 NIR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
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A48754
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Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cipate: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
Cipate: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
Cipate: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
Cipate: 14-Feb-1997 #sequence_revision 13-Mar-1996
A; Taylor, M.S.; Peterson, J.A.; Ceriani, R.L.; Couto, J.R.
Biochim. Biophys. Acta 1306, 1-4, 1996
A; Title: Cloning and sequence analysis of human butyrophilin reveals a potential rece
A; Reference number: S70587; MUID:96201696; PMID:8611614
A; Accession: S70587
A; Molecule type: mRNA
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 25-Feb-1985 sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
C;Accession: B43045; A03792; S33058
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr vi
A;Reference number: A93065; MUID:85035713; PMID:6092825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-221 <BAN>
A;Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24809.1; PID:g1334917
R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.
Nature 310, 207-211, 1984
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8
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A;Contents: annotation; protein coding region
C;Superfamily: human herpesvirus 4 BARFI protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: U39576; NID: 91326082; PIDN: AAC50489.1; PID: 91326083
                                                                                                                              59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
                                                                                                                                                                                                                                                                               | : : : | : : : | | 134 PSKPEIVSKALFLETEQLKKLGDCISEDSYPDGNITWYRNGKVLHPLEGAVVIIFKKEMD 193
                                                                                                                                                                                    84 PEYKDR--LNLSENYTLSISNARISDEKRFVCMLVT-EDNVFEAPTIVKV-----FKQ 133
                                                                                                                                                                                                                                            119 PSISDFE----IPTSNIRRI-ICSTSGGFPEPHLSWLENGEELNAINTTV-----SQD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 YKNRTIFDI---TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEV---TLSV-- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 EVATLSCGHNVSVEELAQTRIYWQK-------EKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 QAVTAFLGERVTLTS----YWRRVSLGPEIEVSWFKLGPGEEQVLIGRMHHDV-IFIE 71
                    DB 2; Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Indels
                 11.6%; Score 133.5; DB 2; 24.5%; Pred. No. 0.0046; tive 35; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 -KADFPTPSISDFEIPTSNIRRIICSTSGGFPEPHLSWL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
11.2%; Score 129; DB 1;
Best Local Similarity 27.0%; Pred. No. 0.0031;
Matches 43; Conservative 25; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BARF1 protein - human herpesvirus 4 (strain B95-8)
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Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                         167 PETELYAVSSKLDFNMT --- TNHSFMCLIKY 194
                                                                                                                                                                                                                                                                                                                                                                                                     194 PVTQLYTMTSTLEYKTTKADIQMPFTCSVTY 224
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27.5%;
Query Match
Best Local Similarity 24.5%;
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R;Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A;Title: Cloning and Sequencing of the rabbit gene encoding T-cell costimulatory molecul A;Reference number: 146689; MUID:95369849; PMID:7642234
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C; Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C; Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C; Accession: 139428
E; Bowen, M.A.; Patel, D.D.; Li, X.; Modrell, B.; Malacko, A.R.; Wang, W.C.; Marquardt, H.J. Exp. Med. 181, 2213-2220, 1995
A; Title: Cloning, mapping, and characterization of activated leukocyte-cell adhesion moley. Reference number: 139428; MUID:95279947; PMID:7760007
              10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD86 precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 23-Jul-1999
           26; Gaps
                                                                                                                                                                        70 TNNLSIVILALRPSDEGTYECVVLKYEK--DAFKREHLAEVTLSVKADFPTPSISDFEIP 127
                                                                                                                                                                                                                 90 RNNWTLRLHNVQIKDMGSYDCFIQKKPPTGSIILQQTLTE--LSVIANFSEPEIKLAQNV 147
                                                                                                                                                                                                                                                                                  128 TSNIR-RIICSTSGGFPEPHLSW--LENGEELNAINTTVSQDPETELYAVSSKLDFNM-- 182
                                                                                                                                                                                                                                                                                                                        72 NLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 RR-----IICSTSGGFPEPHLSWLENGEELNAINTTV------SQDPETELY--AVSS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 TRNSAINLTCSSVQGYPEPKKMFF----VLKTENATTEYDGVIEKSQDNVTGLYNISISG 203
                                                                                              20 ATLSC----GHNVSVEELAQTRIYWQKEKKMVL-----TMMSGDMNIWPEYKNRTIFDI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 EVATLSCGH-NVSVEELAQTRIYWQKEKKMVLTMM----SGDMNIWPEYKNRTIFDITN- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:D49842; NID:g755098; PIDN:BAA08642.1; PID:g755099 C;Superfamily: B7-2 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:L38608; NID:g886257; PIDN:AAB59499.1; PID:g886258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.2%; Score 140.5; DB 2; Length 330; 27.4%; Pred. No. 0.00061;
           43; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 SITFSDDIRNATIXCVL-----QTESTETYSQ-HFP 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 KLDF-NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFP 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
A;Residues: 1-330 <ISO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     183 -TINHSFMCLIKYGHLRVN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 GVWHMTVVCVLETESMKIS 226
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Best Local Similarity 27.48
Matches ,60; qonservative
           Conservative
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        52;
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        Matches
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Search completed: January
Job time: 23 secs
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les 59;
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A; Accession: PS0270
A; Molecule type: protein
A; Residues: 34-48 < TANI>
C; Comment: This protein is uniquely and transiently expressed on spinal cord motoneurons
C; Comment: This protein is uniquely and transiently expressed on spinal cord motoneurons
C; Comment: This protein; transmembrane protein
F;1-37Domain: signal sequence #status predicted <SIG>
F;34-588/Product: adhesion molecule SCI #status predicted <ARRA>
F;500-523/Domain: transmembrane #status predicted <ARRA>
F;101,173,199,271,312,366,462,485,504/Binding site: carbohydrate (Asn) (covalent) #statu
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Neuron 7, 535-545, 1991
A; Title: Molecular cloning and expression of a novel adhesion molecule, SC1.
A; Reference number: JH0506; MUID:92030150; PMID:1931049
A; Accession: JH0506
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Cispecies: Gallus gallus (chicken)
Cispecies: Joun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jul-2000
Cispecies: Joun-1994 #sequence_revision 27-Jul-1994 #text_change 21-Jul-1994 #text_change 21
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10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  adhesion molecule SC1 precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 31-Mar.1992 #sequence_revision 31-Mar-1992 #text_change 21-Jul-2000
C;Accession: JH0506; PS0270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 PS-----ISDFEIPTSNIRRI-ICSTSGGFPEPHLSWLENG-----EELNAINTTVSQ 165
                                                                                                                               42 VGEDAELPCRLSPNASAEHL-ELRWFRKKVSPAVLVHRDGREQEAEQMPEYRGRATLVQD 100
                                                                                                                                                                                                                                      -DITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                            127 PTSNIRRIICSTSGGFPEPHLSW-LENGEELNAINTTVSQDPETE-LYAVSSKLDFNMTT 184
                                                                          16 VKEVATLSC--GHNVSVEELAQTRIYWQKEKKMVLTMMSG---DMNIWPEYKNRTIF--- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:S63276; NID:9238000; PIDN:AAB20170.1; PID:9238001
                                                                                                                                                                                                                                                                                       101 GIAKGRVALRIRGVRVSDDGEYTCF---FREDGSYEEAL--VHLKVAALGSDPHIS-MQV
    20;
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        84; Indels
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        33; Mismatches
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        Conservative
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A; Residues: 1-588 <TAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 NHSFMCLIK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 TKNVSCYIQ 221
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A; Status: preliminary
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        52;
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C; Accession: JC5288
R; Yamao, T.; Matozaki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka, Biochem Biochays. Res. Commun. 231, 61-67, 1997
A; Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localizat A; Reference number: JC5287; MUID: 97223399; PMID: 9070220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: DDBJ:D87967; NID:91864012; PIDN:BAA13520.1; PID:91864013 C;Comment: This protein is a glycosylated receptor-like protein and plays a role in cacts as a docking protein and induce translocation of SHP-2 from the cytosol to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 TMMSGDMNIWPEYKNRTIFDIT -- NNL -- SIVILALRPSDEGTYECVVLKYEKDAFKREH 104
                                                                                                                                                                                                                                                                                                                                                                                       119 PS-----EELNAINTRI-ICSTSGGFPEPHLSWLENG-----EELNAINTTVSQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                              90 PDYKDR--LSLSENYTLSIKNARISDEKRFVCMLVT-EDDVSEEPTVVKV-----FKQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SHFCSGV----IHVTKEVKEVA-----TLSCGHNVSVEELAQTRIYWQK---EKKMVL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 SCFCTGVTGKELKVTQPEKSVSVAAGDSTVLNC---TLTSLLPVGPIKWYRGVGQSRLLI 79
                                                                                                                                                                                                                                                                       59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
                                                                                                                                                                                                             Gaps
A;Molecule type; mRNA
Ksesidues: 1-588 <POD.
A;Cross-references: EMBL:X64301; NID:g63087; PIDN:CAA45579.1; PID:g63088
C;Keywords: glycoprotein
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                                                                                                                                                588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 10.7%; Score 122.5; DB 2; Length 1. Similarity 25.7%; Pred. No. 0.036; 39; Conservative 32; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.5%; Score 120.5; DB 2; 25.9%; Pred. No. 0.044; tive 42; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 NRSTGLFTMTSSLQYMPTKEDANAKFTCIVTY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 DPETELYAVSSKLDFNMT---TNHSFMCLIKY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6, 2003, 14:25:30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-509 < YAM>
                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: JC5288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Contents: Brain
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

January 6, 2003, 14:20:25 ; Search time 13 Seconds (without alignments) 689.145 Million cell updates/sec Run on:

US-09-454-651B-23 1149 1 GLSHFCSGVIHVTKEVKEVA.....LRVNQTFNWNTTKQEHFPDN 216

BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P33681 homo sapien	oryc	Q00609 mus musculu	рошо	l homo	2 mus m		P42071 oryctolagus		0	_	_			P16170 xenopus lae	٠.	P13591 homo sapien		P43121 homo sapien	P31836 bos taurus	P18892 bos taurus	P16621 drosophila		P15364 drosophila	96	35 homo sa	90	35 xenopus	CD.	\sim	7 homo sa		mus mus
ΙD	CD80_HUMAN	CD80_RABIT	CD80_MOUSE	CD86_HUMAN	ICOL_HUMAN	CD86_MOUSE	ICOL_MOUSE	CD86_RABIT	C166_MOUSE	C166_HUMAN	BRF1_EBV	BUTY_HUMAN	C166_CHICK	BUTY_MOUSE	NCA1_XENLA	NCA2_HUMAN	NCA1_HUMAN	TCB_FLV	MU18_HUMAN	NCA1_BOVIN	BUTY_BOVIN	LAR_DROME	CXAR_MOUSE	AMAL_DROME	NCA1_RAT	A33_HUMAN	NCA1_CHICK	NCA2_XENLA	NCA2_MOUSE	NCA1_MOUSE	JAM2_HUMAN	NEO1_CHICK	RAGE_MOUSE
DB						7		1	7	-4	П	7	1	Н	Н	Н	Н	Н	1	٦	П	П	П								Н	-	
Length	288	299	306	329	302	309	322	330	583	583	221	526	588	524	1088	761	848	321	646	853	526	2029	365	333	828	319	1091	1092	725	1115	298		403
% Query Match	\vdash	4		15.8	14.0	13.2	13.1	12.2	11.7	11.6	11.2	11.1	10.7	10.4	ö	o.				9.5			9.4	9.4	9.3			9.1			9.0	8.9	
Score		738	261	182	161	152	150.5	140.5	134.5	133,5	129	127	122.5	119	116.5	115	115	110.5	109.5	109.5	109	109	108.5	107.5	106.5	105	105	104	103.5	103.5	103	102	101.5
Result No.	н	7	e	7	ιΩ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P31398 manduca sex P17948 h vascular	P78310 homo sapien Q9qzs7 mus musculu	P04218 rattus norv O9xt56 bos taurus	P35969 mus musculu P53767 rattus norv	P19320 homo sapien Q9r044 rattus norv	P40199 homo sapien P12960 mus musculu	
HEMO_MANSE VGR1_HUMAN	CXAR_HUMAN NPHN_MOUSE	OX2G_RAT JAM1 BOVIN	VGR1_MOUSE	VCA1_HUMAN NPHN_RAT	CEA6_HUMAN	
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413	365	278	1333	739	344) 1
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100	98.5 98.5	8 6 8 6	966	96.5	96	2
3.4 5.5	36	38	40	444	44) *

ALIGNMENTS

OTTOWNENT O	80.	T 01-FB-1994 (Rel. 28, Created) T 01-FB-1994 (Rel. 28, Last sequence update) T 15-XMN-2002 (Rel. 41, Last annotation update)	T lymphocyte activation ant antigen) (CTLA-4 counter-re	CD80 OK CD28LG1 OK CD28LG OK L Homo sapiens (Human).		NCBI_TaxID=96(SEQUENCE FROM N.A. TISSUE-Lymphoid;	MEDLINE	Freeman G.J., Freedman A.S., Segil J.M., Lee G., William J.F., Nadler L.M.;	RT "B7, a new member of the Ig superfamily with unique expression on promotivated and neonlastic R cells ".	RL J. Immunol. 143:2714-2722(1989).		SEQUENCE FROM N.A. MEDLINE=92307753; PubMed=1377173;	RA Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C., Da Pingont B.		encoding	KL immunogenetics 50:1/3-101(1994). RN [3]		<pre>RX MEDLINE=91341422; PubMed=1714935; RA Freeman G.J., Grav G.S., Gimmi C.D., Lombard D.B., Zhou LJ.,</pre>	White M., Fingeroth J.D., Gribben J.G., Nadler L.M.;			RN [4]	MEDLINE=95088403; PubMed=7527824;	RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,	"CD80 (B7) and CD86 (B70) provide similar costimulatory sig	cell proliferation, cytokine production, and generation	RL J. Immunol. 154:97-105(1995). RN [5]		MEDLINE=20125021; PubMed=10661405;	RA IKEMIZU S., GILDETT K.J., Fennelly J.A., COLLINS A.V., Harlos K., Da Jones R V Stuart D T . Davis S J :		Immunity 12:51-60(2000).	N THE COSTIMULATORI SIGNAL ESSENTIAL FOR ON. T CELL PROLIFERATION AND CYTOKINE	
	CDC	12 12 12	SEE	υÖ	ōŏ	0 2	Z Z	24.0	보전	<u>α</u> δ	i izi	nZ i	* *	מא	4 124	it it	K K	×	r r	i eż	<u>r</u>	: rx	24 D	4 124	<u>α</u> ο	4 12	24	24 24	: pc	K 1	מאס	: P4	α , τ	טט	

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207 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 242

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RESULT 2
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                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YKNRTIFQITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ISDFEIPÅSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKNVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES
                                                                                                                                                                                                                                                                                                 InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003600; Ig_like.
Fam; PR00047; Ig. 1.
SMART; SM00409; IG. 1.
Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .)
 PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
                                                                                                                                                                                                                                                                                                                                                                                                  LYMPHOCYTE ACTIVATION ANTIGEN CD80
                                       AND DENDRITIC CELLS.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
SIMILARITY: CONTAINS I IMMUNGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS I IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
DATABASE: NAME=PROW; NOTE=CD guide CD80 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd80.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BA453EE34528B1F4 CRC64;
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IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5e-89;
les 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 NMTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1149;
100.0%; Pred. No. 1.5
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                              EMBL, M83077, AAA58390.1; -...
BMBL, M83072, AAA58390.1; JOINED.
EMBL, M83073, AAA58390.1; JOINED.
EMBL, M83074; AAA58390.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33048 MW;
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                                                                                                                                                                                                                                                         PIR; A45803, A45803.
PDB; 1DR9; 10-JAN-01.
Genew; HGNC:1700; CD80.
MIM; 112203; -.
                                                                                                                                                                                                                                                                                                                                                                           Receptor; 3D-structure.
SIGNAL 1 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 AA;
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35
243
264
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155
50
162
53
89
89
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TRANSMEM
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CARBOHYD
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenetics 42:217-220(1995).
-!- FUNCTION: INVOIVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                 Oryctolagus cuniculus (Rabbit).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBL_TaxID-9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                   T lymphocyte activation antigen CD80 precursor (Activation B7-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-!- SIMILARITY: CONTAINS I IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS I IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and sequencing of the rabbit gene encoding T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.2%; Score 738; DB 1; Lengtn 2>
63.9%; Pred. No. 5.3e-55;
V. matches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LINKED (GLCNAC. . .) (PORT CONTROL CA 4 2 2 3 E 5 C C 9 1 D E 0 C R C 6 4;
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                                                                                       Last sequence update)
Last annotation update)
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; Ig; 1.
SMART; SM004109; IG, 1.
                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
15-JUN-2002 (Rel. 41, Last ann
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HSSP; P33681; 1DR9.
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                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                          costimulatory molecules
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185
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210
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                       CD80_RABIT
P42070;
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CD80_RABIT
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                  149 IGHPDPNVKRIRCSASGGFPEPRLAWMEDGEELNAVNTTVDQDLDTELYSVSSELDFNVT 208
                                                                                                                                                                           -!- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERRAMILY.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                              124 FEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTIVSQDPETELYAVSSKLDFNMT 183
                                                                                                                                          RTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISD 123
                                        29 HFSSGISQVTKSVKEMAALSCDYNISIDELARMRIYWQKDQQMVLSIISGQVEVWPEYKN 88
HFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gray G.S., Freeman G.J., Gimmi C.D., Lombard D.B., Zhou L.J., White M., Fingeroth J.D., Gribben J.G., Nadler L.M.; "Structure, expression, and T cell costimulatory activity of the murine homologue of the human B lymphocyte activation antigen B7."; J. Exp. Med. 174:625-631(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B7.";
Immunogenetics 38:292-295(1993).
-!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
-!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
- LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Selvakumar A., White P.C., Dupont B.; "Genomic organization of the mouse B-lymphocyte activation antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
T lymphocyte activation antigen CD80 precursor (Activation B7-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AR LOCATION: Type I membrane protein. ECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA N STIMULATED MONOCYTES AND NONCIRCULATING B-CELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 NNHSIVCLIKYGELSVSQIFPWSKPKQE 236
                                                                                                                                                                                                                                                                                                                                                                                                                        184 TNHSFMCLIKYGHLRVNQTFNWNTTKQE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93307789; PubMed=7686531;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigen) (B7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- TISSUE SEE
INTERFERON
MALIGNANCI
-!- DEVELOPMEN
ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-B-cell
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Q00609;
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CD80_MOUSE
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161 KRITCFASGGFPKPRFSWLENGRELPGINTTISQDPESELYTISSQLDFNTTRNHTIKCL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 NLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 VTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITN 71
                                                                                    MGD; MGI:101775; CG80.

InterPro; IPR003599; Ig.

InterPro; IPR003606; Ig_MHC.

Pfam; PF00047; ig; 2.

SMART; SM00409; IG, 1.

Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 RRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                               LYMPHOCYTE ACTIVATION ANTIGEN CD80.
                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD86_HUMAN STANDARD; PRT; 329 AA.
P420B1, Q13655;
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
T lymphocyte activation antigen CD86 precursor (Activation B7-2 antigen) (CTLA-4 counter-receptor B7.2) (B70) (FUN-1) (B063).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              58; Indels
                                                                                                                                                                                                                                                                                            IG-HINGE LIKE (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                              1DBADE0931B84C62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-94053735; PubMed=7694363;
Freeman G.J., Gribben J.G., Boussiotis V.A., Ng J.W.,
                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                  IG-LIKE V-TYPE DOMAIN. IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 561;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 IKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 IKYGDAHVSEDFTWEKPPEDP-PDS 244
EMBL; L12589; AAA37240.1; ALT_SEO.
EMBL; L12585; AAA37240.1; JOINED.
EMBL; L12586; AAA37240.1; JOINED.
EMBL; L12587; AAA37240.1; JOINED.
EMBL; L12588; AAA37240.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                              34589 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                       48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 104; Conservative
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                                                               PIR; S17291; S17291.
                                                                                                                                                                                                                                                                                                                                                                                                              306 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                            P33681; 1DR9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                      38
38
38
38
247
269
272
227
227
165
93
                                                                                                                                                                                                                              DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                           Receptor.
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                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD86_HUMAN
                                                                             HSSF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S., Okumura K., Ito D., Azuma M.; ElD80 (B7) and CD86 (B70) provide similar costimulatory signals for T cell proliferation, cytokine production, and generation of CTL."; J. Immunol. 154:97-105(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL FOLE IN THE EARLY EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS, SUCH AS DECIDING BETWEEN IMMNINTY AND ANERGY THAT IS MADE BY T CELLS WITHIN 24 HOURS AFTER ACTIVATION.

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND
                                                                                                                                                                                                                                                                              MEDLINE-99331831; PubMed-7541777; Jellis C.L., Wang S.S., Rennert P., Borriello F., Sharpe A.H., Green N.R., Gray G.S.; Green N.R., Gray G.S.; Genomic organization of the gene coding for the costimulatory human B-lymphocyte antigen B7-2 (CD86)."; Immunogenetics 42:85-89(1995).
Restivo V.A. Jr., Lombard L.A., Gray G.S., Nadler L.M.; "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human cell proliferation."; Science 262:909-911(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION AS CD86.
MEDLINE=94348060; PubMed=7520767;
Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M., Nadler L.M., Wakasa H., Tedder T.F.,
"The B7-2 (B70) costimulatory molecule expressed by monocytes and activated B lymphocytes is the CD86 differentiation antigen.";
Blood 84:1402-1407(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERPAMILY.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-!- DATABASE: NAME=PROW, NOTE=CD guide CD86 entry;
-WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd86.htm".
                                                                                               SEQUENCE OF 7-329 FROM N.A.
MEDLINE-94050123; PubMed=7694153;
Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,
Lania L.L., Somoza C.,
"B70 antigen is a second ligand for CTLA-4 and CD28.";
Nature 366:76-79(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION.
MEDLINE-95088403; PubMed-7527824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: 017722; AAA86473.1;
EMBL: 017717; AAA86473.1; JOINED.
EMBL: 017719; AAA86473.1; JOINED.
EMBL: 017719; AAA86473.1; JOINED.
EMBL; 017719; AAA86473.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L25259; AAA58389.1; -.
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                                                                                                                                                                                                                                         SEQUENCE OF 7-329 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC:1705; CD86.
                                                                                                                                                                                                                                                                  TISSUE-Foreskin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MONOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601020;
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Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;

PROSITE; PS00290; IG_MHC; FALSE_NEG.

SMART;

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10;
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MEDLINE-20465019; PubMed=11007762;
Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K., Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H.,
Hui A., Köhno T., Manoukian R., Whoriskey J.S., Coccia M.A.;
"Characterization of a new human B7-related protein: B7RP-1 is the ligand to the co-stimulatory protein ICOS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRIHQMNSELSVLANFSQPEI----VPIS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIR-----RIICSTSGGFPEP-HLSWLENGEELNAINTTV-----SQDPETELYAVS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 NITENVYINLICSSIHGYPEPKKMSVL----LRTKNSTIEYDGIMQKSQDNVTELYDVS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | | | | : | | : | | | | | | 34 ETADLPCQFANSQNQSLSELV---VFWQDQENLVLNEVYLGKEKFDSVHSKYMGRTSFD- 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 EVATLSC----GHNVSVEELAQTRIYWQKEKKMVLTMM----SGDMNIWPEYKNRTIFDI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     075144; Q9NRQ1; Q9HD18;
15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein G150)
(B7-related protein-1) (B7RP-1).
ICOSL OR B7H2 OR B7RP1 OR KIAA0653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
TISSUB-Dendritic cell;
MEDLINE=20477846; PubMed=11023515;
MRODINE=20477846; PubMed=11023515;
MRONG S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;
"Costimulation of T cells by B7-H2, a B7-like molecule that binds
                                                        LYMPHOCYTE ACTIVATION ANTIGEN CD86.
                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.8%; Score 182; DB 1; Length 329; 29.0%; Pred. No. 3.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71; Indels
                                                                                                                                             GLIKE V-TYPE DOMAIN.
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
POTENTIAL.
N-LINKED (GLCNAC. ...) (POTINED (GLCNAC. ...)) (POTINED (GLCNAC. ...) (POTINED (G
                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
                                                                                                                                CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 3.1e-08; 38; Mismatches 71
                          POTENTIAL
                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 SKLDF --- NMTTNHSFMCLIKYGHLRV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 ISLSVSFPDVTSNMTIFCILETDKTRL 227
                                                                                                                                                                                                                                                                                                                                                                                                         192 192 N-
213 213 N-
27 27 K
329 AA; 37696 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lood 96:2808-2813(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                             244
244
2648
2648
150
150
157
1135
1135
1135
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Receptor.
                                                     CHAIN
DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                        DISULFID
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                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                   CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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DOMAIN
DOMAIN
                          SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFORMED FACUL TO THE TOTAL OF TOTAL 
                                                                                                                                                 Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A., Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART, KIDNEY, LIVER, LUNG, PANCREAS, PLACEWIA, SKRLETAL MUSCLE, BONE MARNOW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES, SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN LYMPH NODES, LEUKOCYTES AND SPLEEN.
TINDICTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY TREATMENT WITH THE ALPHA IN PERIPHERAL BLOOD B-CELLS AND MONOCYTES, WHILE IT S DECREASED IN DENDRITIC CELLS.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- CAUTION: Ref.4 sequence differs from that shown in position 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 5:169-176(1998).
                                                                                                                                                                                                       Jacobs K.A., Collins M.;
Jacobs K.A., Collins M.;
"Identification of GL50, a novel B7-like protein that functionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 2. SMART; SW00409; IG; 1. SMART; SW004009; IG; 1. SMART; SW00410; IG_like; 1. B-cell activation; Immune response; Glycoprotein; Immunoglobulin domain; Signal; Transmembrane; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF199028; AAF34739.1; -.
EMBL; AF289028; AAG01176.1; -.
EMBL; AF216749; AAK16241.1; -.
EMBL; AB014553; BAA31628.1; ALT_SEO.
                                                                                         TISSUE-Leukocyte;
MEDLINE-20126021; PubMed-10657606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              onward for an unknown reason.
                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
MEDLINE=98403880; PubMed=9734811;
Int. Immunol. 12:1439-1447(2000).
                                                                                                                                                                                                                                                                                   binds to ICOS receptor.";
J. Immunol. 164:1653-1657(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AX100595; CAC36465.1; -. 605717; -.
                                                           SEQUENCE FROM N.A. (ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003606; Ig_MHC.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003599; Ig
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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SEQUENCE FROM N.A.

MEDILINE-94065585; PubMed-7504059;

Freeman G.J., Borriello F., Hodes R.J., Reiser H., Gribben J.G.,

Freeman G.J., Borriello F., Hodes R.J., Reiser H., Gribben J.G.,

Ng J.W., Kim J., Goldberg J.M., Hathcock K., Laszlo G., Lombard L.A.,

Ng J.W., Kim J., Goldberg J.M., Sharpe A.H.,

Wang S., Gray G.S., Madler L.M., Sharpe A.H.,

"Murine B7-2, an alternative CTLA4 counter-receptor that costimulates

T cell proliferation and interleukin 2 production.";
                                                                                                                                                                                                                                                                                                                                                                        142 VVSAPHSPSQDELTFTCTSINGYPRPNVYWINKTD----NSLLDQALQNDTVFLNMRGL 196
                                                                                                                                                                                                                                                                                                                                                     64 RTIFD----ITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTP 119
                                                                                                                                                                                                                                                                                                                                                                                                          120 SISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETE-----L 171
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                14 KEVKEV----ATLSCG-HNVSVEELAQTRIYWQ-KEKKMVLT----MMSGDMNIWPEYKN 63
                                                                                                                                                                                                                                                                                                                 Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.; "Differential expression of alternate mB7-2 transcripts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_raxID=10090;
                                                                                                                                N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
GHV -> ESWNLLLLES (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
antigen) (Early T cell costimulatory molecule-1) (ETC-1).
                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                           14.0%; Score 161; DB 1; Length 302; 26.4%; Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                       95; Indels
                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                647934E21B55E34A CRC64;
                                                                CYTOPLASMIC (POTENTIAL).
                                                                             IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 YAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNT 207
                                                                                                                                                                                                                                                                        36; Mismatches
                           COS LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen C., Gault A., Shen L., Nabavi N.;
                                                                                                                        POTENTIAL.
                                                      POTENTIAL
            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96094437; PubMed=7499829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 7-309 FROM N.A. MEDLINE=94230971; PubMed=7513726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exp. Med. 178:2185-2192(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunol. 155:5490-5497(1995).
                                                                                                                                                                                                                  33349 MW;
                                                                                                                                                                                                                                                                         57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                         302
256
277
3302
3302
1120
223
113
103
1137
1173
302
Alternative splicing.
SIGNAL 18
                                                                                                                                                                                                                                                             Similarity
                         19
257
278
30
151
37
158
137
1137
1137
186
302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD86_MOUSE
P42082;
                                      DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                     VARSPLIC
SEQUENCE
                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                              CARBOHYD
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                                                                                                                                                                                                                                                             Local
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                            CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                       THE COSTIMULATOR RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR I LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY BINDING GD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE BARLY EVENTS OI T CELL ACTIVATION AND COSTIMULATION OF NAYVE T CELLS, SUCH AS ECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T SUBCELLUMAR LOCATION: TYPE I membrane protein.

TISSUE SIGLIFICITY: EXPRESSED ON ACTIVATED B CELLS.

SIMILARIY: GONTAINS I IMMUNOGLOBULIN SUPERFAMILY.

SIMILARIY: CONTAINS I IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

SIMILARIY: CONTAINS I MMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

SIMILARIY: CONTAINS I MMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T LYMPHOCYTE ACTIVATION ANTIGEN CD86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning and expression of early T cell costimulatory molecule-1 and its characterization as B7-2 molecule."; J. Immunol. 15:4929-4936(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8F58DCD1FB81D5EA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG-LIKE V-TYPE DOMAIN. IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC52336.1; ALT_INIT.
AAC52386.1; JOINED.
AAC52336.1; JOINED.
AAC52336.1; JOINED.
AAC52336.1; JOINED.
AAC52336.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00290; IG_MHC; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC52336.1; JOINED.
AAB30744.2; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC52334.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34665 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L25606; AAA79770.1; -. EMBL; U39456; AAC52334.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:101773; Cd86.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00406; IGV;
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146
154
175
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231
309 AA;
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245
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266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; #39465; PEMBL; S70108; P
                                                                                                                                                                                                                                                                                             -!- SUBCELLUIA
-!- TISSUE SIE
-!- SIMILARITY
-!- SIMILARITY
-!- CAUTION: I
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U39462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor.
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EMBL;
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SEQUENCE FROM N.A. (ISOFORM 1).
STRARM-213HH943, TISSBE-FECAL thymus;
MEDILINE-20126021; PubMed=10657606;
Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,
Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,
Jacobs K.A., Collins M.;
"identification of GL50, a novel B7-like protein that functionally
                                                                                                      70 TNNLSIVILALRPSDEGTYECVVLKYEK--DAFKREHLAEVTLSVKADFPTPSISDFEIP 127
                                                                                                                                                                          90 RNNWTLRLHNVQIKDMGSYDCFIQKKPPTGSIILQQTLTE--LSVIANFSEPEIKLAQNV 147
                                                                                                                                                                                                                                                     128 TSNIR-RIICSTSGGFPEPHLSW--LENGEELNAINTTVSQDPETELYAVSSKLDFNM-- 182
                                                                                                                                                                                                                                                                                               TISSUE-Lymphocytes;
MEDLINE=20083495; PubMed=10617205;
Voshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
Brankow D., Campbell P., Chang D., Chiu L., Dai T., Duncan G.,
Brankow D., Campbell P., Chang D., Chiu L., Sai T., Duncan G.,
Elliott G.S., Hui A., Mccabe S.M., Scully S., Shahinian A.,
Shaklee C.L., Van G., Mak T.W., Senaldi G.;
MT-cell co-stimulation through B7RP-1 and ICOS.";
Nature 402:827-832(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Thymus;
MEDLINE-20015817; PubMed-10549624;
Swallow M.M., Wallin J.J., Sha W.C.;
"BTh, a novel costimulatory homolog of B7.1 and B7.2, is induced by TNFalpha.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein G150)
160S Lelated protein-1) (B7RP-1) (LICOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collins M.; Differential expression of inducible costimulator-ligand splice variants: lymphoid regulation of mouse g150-b and human g150 molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ling V., Wu P.W., Miyashiro J.S., Marusic S., Finnerty H.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 AA
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TISSUE-Peripheral blood lymphocytes;
MEDLINE-21286479; PubMed=11390480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binds to ICOS receptor.";
J. Immunol. 164:1653-1657(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunol. 166:7300-7308(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                 183 -TTNHSFMCLIKYGHLRVN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 GVWHMTVVCVLETESMKIS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [mmunity 11:423-432(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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Q9JHJ8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICOL_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
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Conservative

52;

Matches

Similarity

Query Match

Best Local

10;

Gaps

us-09-454-651b-23.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2/B;
ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: ISOFORM I HIGHEST EXPRESSION IN LYMPHOID
TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES
(PARTICULARLY IN THE CORTEX AND IN BOTH PRIMARY AND SECONDARY
FOLLICLES), THYMUS (PREDOMINANILY IN THE MEDULLA) AND PEYER'S
PATCHES (MOSTLY IN THE FOLLICLES), LOWER LEVELS IN MANY
NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG,
SKELETAL MUSCLE AND TESTIS. PRESENY ON FRESHLY ISOLATED SPLENIC B-
ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.
-1- DEVELOPMENTAL STAGE: DETECTED EARLY IN HEMOPOLESIS: IN THE YOLK
Patent number W00121796, 29-MAR-2001.
-!- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
                                                                                    MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY COSTIMULATING MEMORY T CELL FUNCTION DURING PREGNANCY, MAY FUNCTION TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMONOPROPECTIVE
                                                                                                                                                                                                                                                                                                                                                                                                    SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT
                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BIN/MOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .) (POTENTIAL).
HA -> TWAPVPYQDYLIPRYLMSPCLKTRGLP (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [mmunoglobulin domain; Signal; Transmembrane; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!-SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
-!-SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
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IG-LIKE C2-TYPE DOMAIN.
POLY-LEU.
POLY-ALA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY.
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N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig.MHC.
InterPro; IPR003600; Ig_like.
Ffam; PF00047; Ig. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1354701; Icosl.
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                                                                                                                                                           TH2 PHENOTYPE.
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DOMAIN
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                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COSTINUISATION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL Immunogenetics 42:77-220 (1995).

-!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY BINDING CD28 OR CTLA-4, MAY PLAY A CRITICAL FOLE IN THE EARLY EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS, SUCH AS DECIDING BETWEEN IMMUNITY AND ANDROY THAT IS MADE BY T CELLS WITHIN 24 HOURS AFTER ACTIVATION.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBLARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-!- SIMILARITY: CONTAINS I IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                93 PYKSPGINVDSSYKNRGHLSLDSMKQGNFSLYLKNVTPQDTQEFTCRV--FMNTATELVK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                 209 TALQNNTVYLNKLGLYDVISTLRLPWTSRGDVLCCVENVALHQNITSISQAESFTGNNTK 268
                                                                                                                                                                                                                                                                                                                     105 LAE--VTLSVKADFPTP--SISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAIN 160
                                                                                                                                                                                                                                                                                                                                                               151 ILEEVVRLRVAANFSTPVISTSDSSNPGQE-RTYTCMSKNGYPEPNLYWI-NTTDNSLID 208
                                                                                                                                                                                                                                  49 TMMSGDMNIWPEYKNRTIFDITN----NLSIVILALRPSDEGTYECVVLKYEKDAFKREH 104
                                                                                                           Gaps
                                                                                                                                                2 LSHFC--SGVIHVTKEVKEVATLSCGHNVSVE-----ELAQTRIYWQKEKKMV----L 48
                                                                                                                                                                                      38 LSSLCAASAETEVGAMYGSNVVLSC----IDPHRRHFNLSGLYVYWQIENPEVSVTYYL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
SMART; SMO0406; IGv. 1.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                         161 TTVSQDP----ETELYAVSSKLDFNMTTNHSFMCLIKYGHLRVN------QTFNMNTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
R -> H (IN REF. 4 AND 5; CAC36464).
55CCBA4AD12E47E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
B lymphocyte activation antigen CD86 precursor (Activation B7-2
                                                                                                         41;
                                                               Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and sequencing of the rabbit gene encoding T-cell
                                                                                                       32; Mismatches 102; Indels
                                                               DB 1;
                                                             Score 150.5; DB 1
Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=B/J X CHBB:HM;
MEDLINE=95369849; PubMed=7642234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
                   35960 MW;
                                                               13.18; 27.18;
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                                                                                                         65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          costimulatory molecules.
                     322 AA;
                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ., Seto A.;
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                     SEQUENCE
  CONFLICT
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CD86_RABIT
                                                                                                         Matches
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POTENTIAL.

22

SIGNAL

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ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E7BAFA8FCA8F9489 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.7%; Score 134.5; DB 1
25.2%; Pred. No. 0.00063;
Live 34; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSGQKT -> AAGIPA
S -> F (IN REF. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | |:|| |:| |:: |: | BGTQLYTVTSSLEYKTTRSDIQMPFTCSVTY 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PETELYAVSSKLDFNMTTNH---SFMCLIKY 194
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Best Local Similarity 25.2%
Matches 38; Conservative
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1157
2270
3354
4354
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DOMAIN
TRANSMEM
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DISULFID
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CARBOHYD
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CARBOHYD
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C166_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPTSNI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 RR----IICSTSGGFPEPHLSWLENGEELNAINTTV-----SQDPETELY--AVSS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 TRNSAINLTCSSVQGYPEPKKMFF----VLKTENATTEYDGVIEKSQDNVTGLYNISISG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                              EVATLSCGH-NVSVEELAQTRIYWQKEKKMVLTMM----SGDMNIWPEYKNRTIFDITN- 71
                                                                                                                                                                                                                                                                                                                                                                                                                34 KTADLPCQFTNSQSRSLSELVVFWQDQERLVLYELFLGREKPDNVDPKYIGRTSFDQESW 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C166_MOUSE STANDARD; PRT; 583 AA.

Q61490; O70136;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
CD166 antigen precursor (Activated leukocyte-cell adhesion molecule)
                                              CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
POTENTIAL.
POTENTIAL.
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
   LYMPHOCYTE ACTIVATION ANTIGEN CD86.
                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                         Score 140.5; DB 1, __
Dred. No. 9.7e-05;
A. indels 41;
                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 KLDF-NMTINHSFMCLIKYGHLRVNQTFNWNTTKQEHFP 214
                                                                                                                                                                                                                                                                                                                            ; Pred. No. 9.7e 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97353242; PubMed=9209500;
                                                                                                                                                                                                                                                                           37142 MW;
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                                                                                                                                                                                                                                                                                                            12.2%;
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Best Local Similarity z/...
Fest G0; Conservative ?
                                                                                                                                                                                                                                                                                                                              27.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                       192
198
213
330 AA;
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23
23
248
269
269
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150
157
1146
1146
1177
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SEQUENCE
                 DOMAIN
TRANSMEM
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DISULFID
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CARBOHYD
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                                                                       DOMAIN
                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 PEYKDR--LSLSENYTLSIANAKISDEKRFVCMLVT-EDNVFEAPTLVKV-----FKQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : ::: | ::: | : ::| | : | 134 PSKPEIVNKAPFLETDQLKKLGDCISRDSYPDGNITWYRNGKVLQPVEGEVAILFKKEID 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 PSISDFE----IPTSNIRRI-ICSTSGGFPEPHLSWLENGEELNAINTTVS-----QD 166
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IG-LIKE V-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 3.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; Q13740; 1KJC.

MGD; MGI:1313266; Alcam.
InterPro; IPR0033006; Ig_MRC.
InterPro; IPR0033600; Ig_MRC.
Pfam; PF00047; ig; 5.
SMART; SM00410; IG_like; 2.
SMART; SM00410; IG_like; 2.
PROSITE; PS00290; IG_MRC; FALSE_NEG.
Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
THE NERVOUS SYSTEM.
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- SUBLARITY: BELONGS TO THE IMMUNGLOBULIN SUPERFAMILY.
--- SIMILARITY: CONTAINS 3 IMMUNGLOBULIN-LIKE G2-TYPE DOMAINS.
--- SIMILARITY: CONTAINS 2 IMMUNGLOBULIN-LIKE V-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 583;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein Sci. 4:1644-1647(1995).

-I- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN NEDRITE EXTENSION BY NEURONS VIA HETRROPHILIC AND HOMOPHILIC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO ACTIVARED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF THE NERVOUS SYSTEM.

-I- SUBCELLOLAR LOCATION: Type I membrane protein.

-I- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN SUPERFAMILY.

-I- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

-I- DATABASE: NAME-PROW; NOTE-CD guide CD166 entry;

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd166.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ^{\rm MEMD}, a new cell adhesion molecule in metastasizing human melanoma cell lines, is identical to ALCAM (activated leukocyte cell adhesion
                                013740; 060892;
01-NOV-1997 (Rel. 35, Last sequence update)
10-NOV-1997 (Rel. 35, Last annotation update)
CD166 antigen precursor (Activated leukocyte-cell adhesion molecule)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95279947; PubMed=7760007; Bowen M.A., Patel D.D., Li X., Modrell B., Malacko A.R., Bowen M.A., Patel D.D., Li X., Modrell B., Marguardt H., Neubauer M., Pesando J.M., Francke U., Haynes B.F., Aruffo A.; "Cloning, mapping, and characterization of activated leukocyte-cell adhesion molecule (ALCAM), a CD6 ligand."; Exp. Med. 181:2213-2220(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skonier J.E., Bowen M.A., Emswiler J., Aruffo A., Bajorath J.; "Recognition of diverse proteins by members of the immunoglobulin superfamily: delineation of the receptor binding site in the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bajorath J., Bowen M.A., Aruffo A.; "Molecular model of the N-terminal receptor-binding domain of the human CD6 ligand ALCAM.";
                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 2-583 FROM N.A.
MEDLINE=98161527; Pubmed=9502422;
Degen W.G., van Kempen L.C., Gijzen E.G., van Groningen J.J.,
van Kooyk Y., Bloemers H.P., Swart G.W.;
583 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 35:12287-12291(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD6-BINDING DOMAINS.
MEDLINE-96420463; PubMed=8823162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3D-STRUCTURE MODELING OF 28-133.
MEDLINE-96060095; PubMed-8520490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Pathol. 152:805-813(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L38608; AAB59499.1; -. EMBL; Y10183; CAA71256.1; -. PDB; 1KJC; 03-APR-96.
       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligand ALCAM."
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                               ALCAM OR MEMD
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                                                                                                                                                                                                                  (ALCAM)
       HERE THE SECOND COORD CO
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InterPro; IPR003599; Ig. InterPro; IPR003006; Ig_MHC. InterPro; IPR003600; Ig_like.

Genew; HGNC:400; ALCAM.

601662;

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'DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
                                                                                                                                                                                                                                                                                                                                                                                                                             84 PEYKDR--LNLSENYTLSISNARISDEKRFVCMLVT-EDNVFEAPTIVKV-----FKQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 PSISDFE----IPTSNIRRI-ICSTSGGFPEPHLSWLENGEELNAINTTV-----SQD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 PSKPEIVSKALFLETEQLKKLGDCISEDSYPDGNITWYRNGKVLHPLEGAVVIIFKKEMD 193
Pfam; PF00047; ig; 5.
SMART: SW00409; IG; 2.
SMART; SW00410; IG_like; 2.
PROSITE: PS00290; IG_MHC; FALSE_NEG.
Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-84270667; PubMed-6087149;
Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.;
                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Epstein-barr virus (strain B95-8) (Human herpesvirus 4). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.
                                                                                                  CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 3.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                           /FTId=VAR_003908.
E023FB3974A60284 CRC64;
                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                     (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                        11.6%; Score 133.5; DB 1
24.5%; Pred. No. 0.00076;
tive 35; Mismatches 54
                                                                                                                                                                                                                                     (GLCNAC.
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                                                                                                                                                                                                                             (GLCNAC.
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                                                                                                                                                                                                                                                                                         (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                      /FTId=VAR_003907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 AA.
                                                   Repeat; Signal; 3D-structure; Polymorphism. SIGNAL 1 27 POTENTIAL. CHAIN 28 583 CD166 ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PETELYAVSSKLDFNMT---TNHSFMCLIKY 194
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N-LINKED
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                                                                                                                                                                                                                                                                                                                                                    583 AA;
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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457
480
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347
428
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1157
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306
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P03228;
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Best Local Similarity 27.0%; Pred. No. 0.00054;
Matches 43; Conservative 25; Mismatches 47; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YKNRTIFDI---TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEV---TLSV-- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96201696; Pubmed-8611614;

Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.;

Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.;

Taylor M.R., Sequence analysis of human butyrophilin reveals a potential receptor function.";

Biochim. Biophys. Acta 1306:1-4(1996).

-!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA MEMBRANE (BY SIMILARITY).

-!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 EVATLSCGHNVSVEELAQTRIYWQK-------EKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 QAVTAFLGERVTLTS-----YWRRVSLGPEIEVSWFKLGPGEEQVLIGRMHDV-IFIE 71
                                                                                                                                         Wei M.X., Ooka T.; "A transforming function of the BARF1 gene encoded by Epstein-Barr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human),
transparata (Lauratta) (Homan),
transparata (Human),
transparata (Humanalia; Humanalia; Humana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24471 MW; CA5A24D1EA28758E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 -KADFPTPSISDFEIPTSNIRRIICSTSGGFPEPHLSWL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 ERSQFP----DFSVLT-----VTCTVNAFPHPHVQWL 159
                                                                                                                                                                                                                                                                                     -! - FUNCTION: BARF1 HAS TRANSFORMING ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NoV-1997 (Rel. 35, Created)
01-NoV-1997 (Rel. 35, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Butyrophilin precursor (BT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              526 AA.
                                                                        IDENTIFICATION OF PROTEIN.
MEDLINE=90059873; Pubmed=2555151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; V01555; CAA24809.1; -. PIR; A07792; OQBE48. PIR; S33058; S33058. InterPro; IPR003600; Ig_like. SMART; SM0410; IG_like; 1. Early protein; Oncogene. SEQUENCE 221 AA; 24471 MW;
                                                                                                                                                                                                                                              8:2897-2903(1989).
Nature 310:207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Q13410;
                                                                                                                                                                                                             virus.";
                                                                                                                                                                                                                                                 EMBO J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 GIAKGRVALRIRGVRVSDDGEYTCF---FREDGSYEEAL--VHLKVAALGSDPHIS-MQV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 VGEDAELPCRLSPNASAEHL-ELRWFRKKVSPAVLVHRDGREQEAEQMPEYRGRATLVQD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 -DITHNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFFTFSISDFEI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 PTSNIRRIICSTSGGFPEPHLSW-LENGEELNAINTTVSQDPFTE-LYAVSSKLDFNMTT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 VKEVATLSC--GHNVSVEELAQTRIYWQKEKKMVLTMMSG---DMNIWPEYKNRTIF--- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
CD166 antigen precursor (SCI glycoprotein) (BEN glycoprotein) (DM-GRASP protein) (JC7 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                               CITOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
E9ECAOCFBDAF94D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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MEDLINE=92030150; PubMed=1931049;
Tanaka H., Matsui T., Agata A., Tomura M., Kubota I.,
McFarland K.C., Kohr B., Lee A., Phillips H.S., Shelton D.L.;
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.1%; Score 127; DB 1; Length 526; Best Local Similarity 27.5%; Pred. No. 0.0024; Matches 52; Conservative 33; Mismatches 84; Indels 2
                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin domain; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  588 AA.
                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                 BUTYROPHILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 34-53.
                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                            MIM, 601610; -...
InterPro; IPR001870; Gamma_carbxylse.
InterPro; IPR003006; Ig_MHG.
InterPro; IPR003306; Ig_VHG.
InterPro; IPR003878; SPRY_receptor.
InterPro; IPR003877; SPRY_receptor.
Pfan; PF00642; SPRY; 1.
SMART; SM004406; IGY; 1.
SMART; SM004406; IGY; 1.
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27 26
27 242
3 269
3 269
526
526
53004 MW; 1
                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Glycoprotein; SIGNAL 1 26
                                                                                                                                                                EMBL; U39576; AAC50489.1; -.
                                                                                                                                                                                Genew; HGNC:1135; BTN1A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  243
270
55
215
215
526 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C166_CHICK
P42292;
                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=9211411; bubwed=1313497;
Pourquie O., Hallonet M.E.R., le Douarin N.M.;
Pascotation of BEN 91ycoprotein expression with climbing fiber
"Association of BEN 91ycoprotein expression with climbing fiber
avian cerebellum.";
J. Neurosci. 12:1548-1557(1992).
-!-FUNCTION: HOWOPHILIC ADHESION MOLECULE ASSOCIATED WITH CLIMBING
FIBER AXONOGENESIS. SUPPORTS NEURITE EXTENSION.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR CORATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED POPULATION OF AXONS.
WITHIN THE SPINAL CORD IT IS LOCALIZED TO AXONS IN THE DORSAL.
FUNICULUS, MIDLINE FLOOR PLATE CELLS, AND MOTONEURON: FOUND IN
EPITHELIA, CENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH
DEVELOPING SYSTEM CARRIES DIFFERENTLY GLYCOSYLATED MOLECULAR FORMS
"Molecular cloning and expression of a novel adhesion molecule, SC1."; Neuron 7:535-545(1991).
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 34-52; 87-93; 504-512 AND 569-582. TISSUE=Bursa of fabricius;
MEDLINE=9230224; PubMed=1608932;
MEDLINE=9230224; PubMed=1608932;
Pourquie O., Corbel C., le Caer J.-P., Rossier J., le Douarin N.M.;
"BEN, a surface glycoprotein of the immunoglobulin superfamily, is expressed in a variety of developing systems.";
Proc. Natl. Acad. Sci. U.S.A. 89:5261-5265(1992).
                                                                                                                                                                                                                       DM-GRASP, a novel immunoglobulin superfamily axonal surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00290; IG_MHC; FALSE_NEG.
Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE: WIDELY EXPRESSED DURING EMBRYONIC
                                                                                                                                                             Burns F.R., von Kannen S., Guy L., Raper J.A., Kamholz J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG-LIKE V-TYPE DOMAIN 1.
IG-LIKE V-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 3.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD166 ANTIGEN.
                                                                                                                                                                                                                                                        that supports neurite extension."; Neuron 7:209-220(1991).
                                                                                                                                MEDLINE=91337449; PubMed=1873027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, S63276; AAB20170.1; -.
EMBL; M76678; AAA48602.1; -.
EMBL; X64301; CAA45579.1; -.
HSSP; Q13740; IKJC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00409; IG; 3.
SMART; SM00410; IG_like; 2.
                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POSSIBLE FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENT.
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         HERETERERANDER PRESENTATION OF THE PRESENT OF THE P
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59 PEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPT 118
                                                                                                                                                                                                                                                                                                                                                               119 PS-----ISDFEIPTSNIRRI-ICSTSGGFPEPHLSWLENG-----EELNAINTTVSQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochim. Biothy Acta 1245:285-292(1995).

-! FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA MEMBRANE (BY SIMILARITY).

-! SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE.

-! SUBCELLULAR LOCATION: Type I membrane protein.

-! TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ishii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda T.; "Carboxy-terminal tytoplasmic domain of mouse butyrophilin specifically associates with a 150-kpa protein of mammary epithelial cells and milk fat globule membrane.";
                                                                                                                                                                                                                                                                                 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                         (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL).
(POTENTIAL).
                                                    (POTENTIAL).
                                                                                                                                                            (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0gg\ S.L.,\ Komaragiri\ M.V.S.,\ Mather\ I.H.; "Structural organization and mammary-specific expression of the
                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                      DB 1; Length 588;
                                                                                                                                                                                                                                                    10.7%; Score 122.5; DB 1; Length 5 25.7%; Pred. No. 0.0065; tive 32; Mismatches 54; Indels
                                                                                                                                                                                                              ) -> HK (IN REF. 2).
2A28612D0164531E CRC64;
                                                                                                                                                          MMEPPAAAAR -> MEPPSRRRP
A -> S (IN REF. 3).
SD -> RH (IN REF. 3).
                                   N-LINKED (GLCNAC...) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BUTY_MOUSE STANDARD; PRT; 524 AA. 062556; P97392; 01-NOV-1997 (Rel. 35, Created) 1-NUL-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Butyrophilin precursor (BT).
                                                                                                                                                                                                A -> T (IN REF.
LQ -> HK (IN RE
                                                                                                                                                                                                                                                                                                                                                                                                                                      : | |: :: | | : | | 199 NRSTGLFTMTSSLQYMPTKEDANAKFTCIVTY 230
                                                                                                                                                                                                                                                                                                                                                                                                                     166 DPETELYAVSSKLDFNMT---TNHSFMCLIKY 194
                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129; TISSUE=Mammary gland;
MEDLINE=97148936; PubMed=8995761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Mammary gland;
MEDLINE=96125722; PubMed=8541302;
                                                                                                                                                                                                                              65726 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             butyrophilin gene.";
Mamm. Genome 7:900-905(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 39-487 FROM N.A.
                                                                                                                                                                                                                                                                     1 Similarity 25.79 39; Conservative
3319
3319
1101
1101
1103
1109
104
504
462
504
100
100
101
329
                                                                                                                                                                                                                              588 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
276
359
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1101
1173
1199
271
312
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112
329
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                                                                                                                                               CARBOHYD
CONFLICT
CONFLICT
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CARBOHYD
DISULFID
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                          DISULFID
                                                                                                                                  CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                 CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

D -> DD (IN REF. 2).

E -> D (IN REF. 2).

E -> D (IN REF. 2).

Y -> E (IN REF. 2).

SL -> FF (IN REF. 2).

DIPLSPLGEGCTSGDKDT -> GHSLVPAGGRLYFWRQRH
          DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF OF PREGNANCY AND IS MAXIMAL DURING LACTATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 ITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSISDFEIPT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSF 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 ATLSCGH--NVSVEELAQTRIYWQKEKKMVLTMMSGD-----MNIWPEYKNR----TIFD 68
 ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.
                              SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BIN/MOG
                                                 SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.4%; Score 119; DB 1; Length 524; 23.8%; Pred. No. 0.011; tive 34; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                 Immunoglobulin domain; Signal.
                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333F4DE2C7704480 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1088 AA.
                                                                                                                                                                                                                                                                                                     BUTYROPHILIN.
                                                                                                                                                                         MGD; MGI:103118; Brhal.
InterPro; IPR001870; Gamma_carbxylse.
InterPro; IPR001870; Gamma_carbxylse.
InterPro; IPR003878; SPRV_domain.
InterPro; IPR003878; SPRY_comain.
InterPro; IPR003877; SPRY_receptor.
Pfam; PR0047; ig; 1.
Pfam; PR0062; SPRY; 1.
SMART; SM00406; IGV; 1.
SMART; SM00446; SPRY; 1.
Transmembrane; Glycoprotein; Immunoglobustant.
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                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCAl_XENLA STANDARD;
P16170;
01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58406 MW;
                                                                                                                                                     EMBL; U67065; AAB51034.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52# AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 MCLIK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 SCCIQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
DOMAIN
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SUBCELLUIAR LOCATION: Type I membrane protein.
-:- ALTERNATUR PRODUCTS: 2 isoforms, N-CAM 180 (shown here) and
N-CAM 140; are produced by alternative splicing.
-:- IISSUE SPECIFICITY: EXPRESSED IN NEURON AND IN PRESUMPTIVE NEURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEURAL CELL ADHESION MOLECULE 1, 180 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING EARLY NEURAL DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                            molecule (NCAM).";
Nucleic Acids Res. 17:10321-10335(1989).
-!- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM
                                                                                                                           Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDIINE=90098871; PubMed=2481269;
Krieg P.A., Sakaguchi D.S., Kintner C.R.;
"Primary structure and developmental expression of a large cytoplasmic domain form of Xenopus laevis neural cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M25696; AAA49909.1; -.
PIS; S09600; IJXLNL.
HSSP; P56276; JTLNL.
InterPro; IPR003961; FN_III.
InterPro; IPR003961; Ig_C2.
Pfam; PF00041; fins; 2.
Pfam; PF00041; fins; 2.
Pfam; PR00060; FN3; 2.
SMART; SM00408; IGG2; 5.
Cell adhesion; GIgoprotein; Transmembrane; Repeat; Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 5.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
HEPARIN-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEPARIN-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin domain; Alternative splicing; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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1088
1088
100
193
289
289
589
686
153
162
186
285
283
379
                                                                                                                                                                                                      Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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6
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                                                                                                                                                     Query Match
10.1%; Score 116.5; DB 1; Length 1088;
Best Local Similarity 24.0%; Pred. No. 0.044;
Matches 43; Conservative 31; Mismatches 58; Indels 47; Gaps
                                                                                                                                                                                            18 EVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITNNLSIVI 77
                                                                                                                                                                                                                      134 -IICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN-----MTTNH 186
                                                                                                                                                                                                                                 228 VVLSCDADGFPDPEISWLKKGEPI------EDGE------EKISFNEDQSEMTIHH 271
Search completed: January 6, 2003, 14:24:26
Job time: 15 secs
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1149
1 GLSHFCSGVIHVTKEVKEVA......LRVNQTFNWNTTKQEHFPDN 216
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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2: sp_bacteria:*
3: sp_tungi:*
4: sp_tungi:*
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Maximum DB seq length: 200000000
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Perfect score:
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4: sp_human:*
5: sp_invertebrate:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_organealle:*
9: sp_phage:*
10: sp_phage:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_uniclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					COLUMNITOS	
Result	ı	Query	:		;	
일 :	Score	Match	Match Length DB	8	ID	Description
1	1118	97.3		9	077684	077684 macaca neme
7	1100	95.7		9	028499	Q28499 macaca mula
e	1085	94.4		9	Q9BDN6	Q9bdn6 cercocebus
4	1085	94.4		9	028347	Q28347 cercocebus
2	772	67.2		9	Q8WMZ2	Q8wmz2 sus scrofa
9	764	66.5		9	Q9N213	
7	762.5	66.4		9	Q9TT70	Q9tt70 sus scrofa
80	762.5	66.4		9	Q9BE99	Q9be99 sus scrofa
6	761	66.2		9	Q9TT71	Q9tt71 sus scrofa
10	743	64.7		9	Q9GMZ8	Q9gmz8 felis silve
11	743	64.7		9	002758	002758 felis silve
12	719	62.6	304	9	Q9TQX1	Q9tqx1 canis famil
13	717.5	62.4		ø	046405	046405 bos taurus
14	705	61.4		9	010N60	Q9nOtO canis famil
15	705	61.4		9	Q9TQS8	Q9tqs8 canis famil
16	603.5	52.5		11	035187	035187 rattus norv

601.5 52.4 290 11 062680 596 51.9 321 11 055202 560 48.7 30.6 11 055202 350 30.5 174 6 095R129 349.5 30.4 173 6 095R129 200.5 17.4 329 6 095R17 200.5 17.4 332 6 095L16 188.5 16.4 296 13 042404 1188.5 16.4 296 13 042404 1188.5 16.4 296 13 042404 17 15.4 323 6 095R16 17 15.4 323 6 095R04 17 15.3 323 6 095R04 18.3 323 6 095R24 18.4 325 6 002838 18.5 334 11 035R31 15.3 13.3 356 11 054R21 15.3 13.3 399 11 091R27 15.3 13.3 316 4 095RX1 139.5 12.1 521 6 046651	Q62680 rattus norv Q62624 rattus norv Q55202 rattus norv Q97129 mus musculu Q90mz9 felis silve		78673
552 522 522 522 522 523 523 523	111119		
11. 11.	52.4 52.3 51.9 88.7	3305 22222 177.4 16.4 15.8 15.8	177 15.4 177 15.4 177 15.4 176 15.3 171 14.9 1.62 14.1 1.69 13.8 16.5 13.6 16.5 13.8 16.5 13.8 16.5 13.8 16.5 13.8 16.5 13.8 16.5 13.8 16.5 13.2 16.5 13.2 1

ALIGNMENTS

			0;	
SUL 768	GN B/. Macaca nemestrina (Pig-tailed macaque). OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; OC Cercopithecinae; Macaca.	RA Kraus G., Hnatyszyn J.H.; RA Kraus G., Hnatyszyn J.H.; Rubmitted (JUL1998) to the EMBL/GenBank/DDBJ databases. Submitted (JUL1998) to the EMBL/GenBank/DDBJ databases. DR RHSSP; P33681; 1DR9. DR InterPro; IPR003599; 1g. DR InterPro; IPR003600; 1g_like. DR InterPro; IPR003600; 1g_MHC. DR RAPER; SM00409; 1G; 1. DR SMART; SM004010; 1G_like; 1. SQ SEQUENCE 288 AA; 33131 MW; 76BBC42839E9AB79 CRC64;	Query Match 97.3%; Score 1118; DB 6; Length 288; Best Local Similarity 97.7%; Pred. No. 1.2e-91; Matches 210; Conservative 1; Mismatches 4; Indels 0; Gaps	Oy 2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61

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             148 TDFEIPPSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDFFTELYTVSSKLDFN 207
122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
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                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                           Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A., "Comparative sequence analysis of cytokine genes from human and
                                                                                                                                                                                                                                                                                                                                                                            Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.;
"Cloning, sequencing and homology analysis of nonhuman primate Fas/Fas-Ligand and co-stimulatory molecules.";
Immunogenetics 0:0-0(2001).
EMBL; AAA86706.1; -.
HSSP; P33681; 1DR9.
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E70BEA4006C7A609 CRC64;
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01, Last sequence update)
21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1100; DB 6;
Pred. No. 4.8e-90;
2; Mismatches 6;
                                                           208 MTINHSFMCLIKYGHLRVNQTFNWNTPKQEHFPDN 242
                                              182 MITNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created 01-NOV-1996 (TrEMBLrel. 01, Last se 01-JUN-2002 (TrEMBLrel. 21, Last an BT protein (CD80 protein precursor) B7 OR N939.
                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                MEDLINE-96003435; PubMed=7561102;
                                                                                                                                                                                                                                                                                                                                  nonhuman primates.";
7. Immunol. 155:3946-3954(1995).
SEQUENCE FROM N.A.
                                                                                                                                                                                                          Macaca mulatta (Rhesus macaque).
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33141 MW;
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Interpro; IPR003600; Ig_like.
Interpro; IPR003006; Ig_MHC.
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Best Local Similarity 96.3%;
Matches 207; Conservative
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                                                                                                                            PRELIMINARY;
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SMART; SM00409; IG; 1.
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                                                                                                                                                                                                                                                      NCBI_TaxID=9544;
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62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
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                                                                                                                                                                                                                                                                            Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey). 
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; 
Cercopithecinae; Cercocebus.
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloining, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules."; immunogenetics 53:315-338(2001).
EMBL; AF344839; AAK37535.1; -.
HSSP; P33681; 1DR9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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MEDLINE-21383618; PubMed-11491535;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
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                                                                                                                         Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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95.3%; Pred. No. 1e-88;
iive 4; Mismatches 6;
    AA.
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288
                                                                               Created)
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MEDLINE=96003435; PubMed=7561102;
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                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 21,
                                                                           01-JUN-2001 (TrEMBLrel. 17,
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Matches 205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weiss W.R., Ansari A.A.;
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                                                                                                                                                                                                 CD80 protein.
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                                     Q9BDN6;
9NGE60
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181 NMTTHISFMCLIKYGHLRVNQTFNWNTTKQE 211 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 | 1:1 |

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Tadaki D.K., Williams A., Iee K.P., Kirk A.D., Harlan D.M.;
Porcine CD80: Cloning, characterization and evidence for its role in direct human T-cell activation.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF455011; AAL58443.1;
InterPro; IPR003559; Ig.
InterPro; IPR003056; Ig.MHC.
Pfam; PF00047; Ig; 2.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                           62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
                                                                                                                                                                                                                                                                                                                 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
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                                                                                                                                                                                                                                                     28 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYCQKEKKMVLTMISGDMNIWPEY 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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                                                                                                                                                                            Length 289;
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                                                                                                                                                                       94.4%; Score 1085; DB 6; Length 2 95.3%; Pred. No. 1e-88; vative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42; Indels
                                                                                                                                          289 AA; 33030 MW; 5ED6A3F6A3C59297 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.2%; Score 772; DB 6; 66.8%; Pred. No. 8.2e-61; ative 28; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                         208 MTTHHSFVCLIKYGHLRVNQTFNWNTPKQEHFPDN 242
                                                                                                                                                                                                                                                                                                                                                                                                                       182 MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 AA
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nonhuman primates.";
J. Immunol. 155:3946-3954(1995).
EMBL; U1983; AAA86700.1; -.
HSSP; P33681; 1DR9.
InterPro; IPR003600; Ig_like.
InterPro; IPR003066; Ig_MHC.
                                                                                      Pfan; PF00047; 1g; 1.
SMART; SM00410; 1G_like; 2.
NON TER 289 289
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                                                                                                                                                                                                       Matches 205; Conservative
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01-MAR-2002
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                                                                                                                                           SEQUENCE
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61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 230;
                                                                                                                                                                                                   STRAIN-LANDBACE; TISSUE-SPLEEN;
Wada M., Amae S., Hoshi M., Nio M., Ohi R.;
Wordine CD80(B-7) mRNB, partial cds.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB026121; BAA90700.2; -...
HISSP; P33681; LDRR9.
InterPro; IPR003599; Ig.
InterPro; IPR003509; Ig.like.
                                                                                                                                                                                                                                                                                                                                                                                                230 POTENTIAL.
26028 MW; EB63AD172663C4A4 CRC64;
                                                                   Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         66.5%; Score 764; DB 6;
67.0%; Pred. No. 3.1e-60;
iive 26; Mismatches 43
                           230 AA
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                                                   01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last seq
01-UTN-2002 (TrEMBLrel. 21, Last ann
CDB0 protein precursor.
                         PRT;
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                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 67.09
Matches 140; Conservative
                           PRELIMINARY;
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30
230 AA;
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                                                                                                                                                               NCBI_TaxID=9823;
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SEQUENCE
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                         Q9N2I3
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Q9TT70
RESULT 6
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NCBI_TaxID=9823;
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Q9TT71;
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SIGNAL
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                   Faas S.J., Glannoni M.A., Matis L.A., Riesecker C.L., Reed D.J., Wu D., Primary Structure and Functional Characterization of a Soluble,
T "Primary Structure and Functional Characterization of a Soluble,
T alternatively Spliced Form of B7-1.";
J. Immunol. 164:6340-6348(2000).
R EMBL; AF203443; AAF22750.1; -.
R INTERPO: IPR003599; IG.
R InterPo: IPR003509; Ig.
R InterPo: IPR003006; Ig_like.
R InterPo: IPR003006; Ig_like.
R SMART; SM00409; IG. 1.
R SMART; SM00410; IG_like; 1.
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                                                                                                                                                                                                                                                                                                                                  61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                                                                                                                                                                                                                                                                                                                                               121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "cloning and sequencing of cDNAs for porcine B7-1 (CD80) and soluble isoforms.";
                                                                                                                                                                                                                                                                                      1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                  22 GLEDECSGIVQVIKTVKEIAVLSCDYNISTEELIRVRIYWQKDNEMVLAVMSGKVKVWPK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metažoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=LANDRACE; TISSUE=ILEUM MUCOSA;
Wada M., Amae S., Sano N., Ishii T., Hoshi M., Sasaki H., Nio M.,
Hayashi Y., Ohi R.;
                                                                                                                                                                                                                                        66.4%; Score 762.5; DB 6; Length 288; 66.5%; Pred. No. 5.5e-60; Live 28; Mismatches 42; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO49760; BAB40952.1; -.
HSSP; P33681; 1DR9.
                                                                                                                                                                                                                  32510 MW; 67E31D0FDB45D1C8 CRC64;
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                                                                                                                                                                                             CD80 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                           181 NMTTNHSFMCLIKYGHLRVNQTFNW-NTTKQE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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           MEDLINE=20302785; PubMed=10843688;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                               Matches 141; Conservative
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30 >288
288 288
288 AA; 325:
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 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                            61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELTRVRIYWQKDNEMVLAVMSGKVKVWPK 81
                                                                                                                      Gaps
                                                                                                                                                                                            22 GLFDFCSGIVQVTKTVKEIAVLSCDYNISTEELTRVRIYWQKDNEMVLAVMSGKVKVWPK 81
                                                                                                                                                                   1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-SPLEEN;
wada M., Amae S., Hoshi M., Nio M., Ishii T., Sano N., Sasaki H.,
Ohi R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                   1;
                                                                        DB 6; Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 66.2%; Score 761; DB 6; Length 229; Best Local Similarity 67.8%; Pred. No. 5.6e-60; Matches 139; Conservative 26; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Splicing Isoform of Porcine CD80.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
REMEL, AF203442; AAF22749.1;
REMEL, AB038153; BAA90764.1;
RESP; P33681; 1DR9.
InterPro; IPR003560; Ig.
InterPro; IPR00360; Ig.like.
InterPro; IPR003006; Ig.MHC.
Pfan, PF00047; Ig; 1.
SMART; SM00410; IG.like; 1.
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C3AD172663C4A4ED CRC64;
30 297 CD80 PROTEIN.
297 AA; 33438 MW; 23109711EA63EF23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                      66.4%; Score 762.5; DB 6;
66.5%; Pred. No. 5.8e-60;
Live 28; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 NMTTNHSFMCLIKYGHLRVNQTFNW-NTTKQE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29
229 CE
25900 MW;
                                                                                                                        Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD80 protein precursor.
CD80 OR CD80/B7-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                        Query Match
Best Local Similarity
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NCBI_TaxID=9615;
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              DR RET DR BE DR BE
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61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPS 120
                         62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-2048532: Pubbmed-11029611;
A Nishimura Y., Shimojima M., Miyazawa T., Sato E., Nakamura K.,
Nishimura Y., Shimojima M., Miyazawa T., Sato E., Nakamura K.,
Izumiya Y., Ikeda Y., Mikani T., Takahashi E.;
A Izumiya Y., Ikeda Y., Mikani T., Takahashi E.;
Izumiya Y., Ikeda Y., Mikani T., Takahashi E.;
A Izumiya Y., Ikeda Y., Mikani T., Takahashi E.;
Inceract with human of Leonon and B7-1 (CD80) and B7-2 (CD86) homologues which
Inceract with human CTLA4-19.";
EMBL; AB030651; BAB11687.1; -.
R HSSP; P38861; IDR9.
R InterPro; IPR003600; Ig_like.
R InterPro; IPR003600; Ig_like.
R InterPro; IPR003600; Ig_like.
R SMART; SM00409; IG; I.
SMART; SM0409; IG; I.
SMART; SM040910; IG; Ilke; Z.
R SMART; SM040910; IG; Ilke; Z.
                                                                                                                121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 AA; 33540 MW; ED9AEECE10D30401 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
B-lymphocyte activation antigen B7-1 (CD80).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.7%; Score 743; DB 6;
63.3%; Pred. No. 3.1e-58;
.ive 33; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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                                                                                                                                                                                                                                                                                                                                          292 AA
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(TrEMBLrel. 04, Last sequ
(TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                             PRT;
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Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9685;
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01-JUL-1997 (
01-JUN-2002 (
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002758;
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002758
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62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
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MEDLINE-20093996; PubMed-10630300;
Yang S., Sim G.-K.;
"New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
Molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY
T-cell specific surface glycoprotein B7-1.
Fells silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 292;
                                                                                                                                                                                            Hash S.M., Collisson E.W.;
"Felis catus t-cell specific surface glycoprotein B7-1.";
"Felis catus t-cell specific surface glycoprotein B7-1.";
EMBL: (1996), Veterinary Pathobiology, Texas A&M Univ.
EMBL: (187755; AAB53575.1; -...
HSSP; P33681: JDR9.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1. SMRT; SM00410; IG_like; 2. SRRUENCE 292 AA; 33482 MW; 6F117E7852B7950F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.7%; Score 743; DB 6; 63.3%; Pred. No. 3.1e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 PEYKNRTIFDITUNLSIVILALRPSDEGTYECVVLKYE-KDAFKREHLAEVTLSVKADFP 117
                                                                                                                                                                                                                                                                                  62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI 121
                                                                                                                                                                                                                                                                                                                                                  122 SDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFN 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 GLFYFCSGITPKSVTKRVKETVMLSCDYNTSTEELTSLRIYWQKDSKMVLAILPGKVQVW 86
                                                                                                                               Gaps
                                                                                                                                                                                                   28 LFYFCSGIIQVNKTVKEVAVLSCDYNISTTELMKVRIYWQKDDEVVLAVTSGQTKVWSKY 87
                                                                                                                                                                       2 LSHFCSGVIHVTKEVKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
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                                                                                 62.6%; Score 719; DB 6; Length 304; 60.5%; Pred. No. 4.4e-56; ative 36; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 25 POTENTIAL.
296 296
296 AA; 33618 MW; 7ADB11FB5F532EF5 CRC64;
                    B7-1 PROTEIN.
09E082F6BB06C94F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 63.2%; Score 717.5; DB 6 Similarity 63.2%; Pred. No. 5.8e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 MTTNHSFMCLIKYGHLRVNQTFNWNTTKQEHFPDN 216
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POTENTIAL
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MEDLINE-99115507; PubMed-9914337;

PATSONS K.R., HOWART C.;

"Cloning of cattle CD80.";

Immunogenetics 49:231-234(1999).

EMBI: Y09950; CAA71081.1; -.

HSSP; P33681; IDR9.

InterPro; IPR003509; Ig.

InterPro; IPR003600; Ig_like.

InterPro; IPR003600; Ig_like.

Pfam: PP00047; ig; 2.

SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD80 anitgen precursor (Fragment).
                                        304 AA; 34454 MW;
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                                                                                                                               Matches 130; Conservative
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33
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                                                                                                          Similarity
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SIGNAL
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Regulator From N.A.

Rhatlani T., Ma Z., Onishi T.;

"Cloning and Sequencing of canine cDNA encoding T-cell co stimulatory molecule B7-1."

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

It submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

Rhatlani APZ5763; APR69006.1; -.

Rhatlani APZ6763; APR69006.1; -.

Richerbo; IPR003569; Ig.

Richerbo; IPR003606; Ig.—ike.

Richerbo; IPR003006; Ig.—ike.

Ream; PF00047; ig. 1.

Ryakr; SM00409; IG. 105; I.

Ryakr; SM00409; IG. 116; I.

Ryakr; SM04010; IG. 116; I.

Ryakr; SM04010; IG. 116; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 ENRTFADFINNLSIVIMALRLSDNGKYTCIVOKTEKRSYKVKHMISVMLLVRADFPVPSI 147
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SEQUENCE FROM N.A.
MEDLINE-20093996; PubMed=10630300;
Yang S., Sim G.-K.;
"New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 LFYFCSGIIQVNKTVKEVAVLSCDYNISTTELMKVRIYWQKDDEVVLAVTSGQTKVWSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 KNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADFPTPSI
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEY
                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
Canis.
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                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Secreted B7-1 protein precursor.
                                                                                                                                                                                                                         01-077-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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178 LDFNMTTNHSFMCLIKYGHLRVNQTFNWNTTK
                       208 ITSNHSFVCLVKYGDLTVSQIFNWQKCK 235
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        SIGNAL
        1
        33
        POTENTIAL.

        CHAIN
        34
        235
        SECRETED B7-1 PROTEIN.

        SEQUENCE
        235
        AA;
        CC08CAA676BCB40A CRC64;

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Job time: 31 secs
                          Immunogenetics 50:349-353(1999).
EMBL; AF106831; AAF17296.1; -
EMBL; AF106831; AAF17294.1; -
EMBL; AF106839; AAF17294.1; JOINED.
EMBL; AF106839; AAF17294.1; JOINED.
EMBL; AF106830; AAF17294.1; JOINED.
INCEPPO: IPR003599; Iq.
INCEPPO: IPR003600; Ig_like.
InterPro: IPR003006; Ig_MHC.
Fam: PF00047; Ig; 1.
SMART; SMO0410; IG_like; 1.
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